

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: Samuel Wei Liu Examiner #: 79120 Date: 5-20-03
 Art Unit: 1653 Phone Number 306-3463 Serial Number: 09297040
 Mail Box and Bldg/Room Location: 9B01 Results Format Preferred (circle): PAPER DISK E-MAIL
9D08

If more than one search is submitted, please prioritize searches in order of need:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

please search peptide sequence SEQ ID NO: 4

Thanks

Samuel Liu

POINT OF CONTACT:
PAUL SCHULWITZ
TECHNICAL INFO. SPECIALIST
CM1 6806 TEL. (703) 305-1954

STAFF USE ONLY**Type of Search****Vendors and cost where applicable**

Searcher: _____	NA Sequence (#) _____	STN _____
Searcher Phone #: _____	AA Sequence (#) <u>1</u>	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>5/20</u>	Bibliographic _____	Dr.Link _____
Date Completed: <u>5/20</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: <u>5</u>	Fulltext _____	Sequence Systems _____
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: <u>5</u>	Other _____	Other (specify) _____

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GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: May 20, 2003, 12:18:40 ; Search time 21 Seconds
(without alignments)
1161.737 Million cell updates/sec

Title: US-09-297-040-4

Perfect score: 1357
Sequence: 1 MADNFSLHDALSGGNPNPQ.....ISKLGISGIDILTSASYMI 246

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 375593 seqs, 99172665 residues

Total number of hits satisfying chosen parameters: 375593

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1315	96.9	250	9	US-09-981-353-127
2	1315	96.9	250	9	US-10-235-674-10
3	1315	96.9	250	9	US-09-877-790-2
4	1315	96.9	250	9	US-10-153-668-346
5	1315	96.9	250	10	US-09-263-689-10
6	1079	79.5	262	9	US-10-235-674-14
7	1079	79.5	262	10	US-09-263-689-14
8	752	55.4	149	9	US-09-728-479-6
9	723	53.3	143	9	US-09-877-790-1
10	295	21.7	322	10	US-09-728-479-11
11	289	21.3	378	9	US-09-854-133-439
12	289	21.3	378	10	US-09-738-973-439
13	283	20.9	323	10	US-09-728-479-2
14	267	19.7	323	10	US-09-728-479-12
15	264	19.5	311	9	US-10-235-674-4
16	264	19.5	311	10	US-09-263-689-4
17	250.5	18.5	145	9	US-10-235-674-12
18	250.5	18.5	145	10	US-09-728-479-8
19	250.5	18.5	145	10	US-09-894-526-5

20	250.5	18.5	145	10	US-09-263-689-12	Sequence 12, Appl
21	249	18.3	149	10	US-09-894-526-3	Sequence 3, Appl
22	246.5	18.2	168	9	US-10-025-380-199	Sequence 199, Appl
23	246.5	18.2	168	10	US-09-922-217-199	Sequence 199, Appl
24	246.5	18.2	168	10	US-09-833-263-199	Sequence 199, Appl
25	243.5	17.9	145	10	US-09-894-526-1	Sequence 1, Appl
26	236.5	17.4	324	9	US-10-235-674-11	Sequence 11, Appl
27	236.5	17.4	324	10	US-09-728-479-7	Sequence 7, Appl
28	236.5	17.4	324	10	US-09-263-689-11	Sequence 11, Appl
29	223.5	16.5	183	9	US-09-948-227-8	Sequence 8, Appl
30	223.5	16.5	200	9	US-10-235-674-8	Sequence 8, Appl
31	223.5	16.5	200	10	US-09-263-689-8	Sequence 8, Appl
32	223.5	16.5	316	10	US-09-747-804-5	Sequence 5, Appl
33	223.5	16.5	317	9	US-10-235-674-6	Sequence 6, Appl
34	223.5	16.5	317	9	US-09-948-227-6	Sequence 6, Appl
35	223.5	16.5	317	10	US-09-263-689-6	Sequence 6, Appl
36	218.5	16.1	315	10	US-09-728-479-10	Sequence 10, Appl
37	218.5	16.1	316	9	US-10-235-674-15	Sequence 15, Appl
38	218.5	16.1	316	9	US-10-235-674-17	Sequence 17, Appl
39	218.5	16.1	316	10	US-09-263-689-15	Sequence 15, Appl
40	218.5	16.1	316	10	US-09-263-689-17	Sequence 17, Appl
41	215.5	15.9	323	9	US-09-981-353-110	Sequence 110, Appl
42	215.5	15.9	323	9	US-10-025-380-1064	Sequence 1064, Ap
43	215.5	15.9	323	9	US-10-235-674-2	Sequence 2, Appl
44	215.5	15.9	323	10	US-09-802-674-2	Sequence 2, Appl
45	215.5	15.9	323	10	US-09-922-217-1064	Sequence 1064, Ap

ALIGNMENTS

RESULT 1
US-09-981-353-127
; Sequence 127, Application US/09981353
; Patent No. US20020160382A1
; GENERAL INFORMATION:
; APPLICANT: Iasek, Amy W.
; APPLICANT: Jones, David A.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981,353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 127
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 898779CD1
US-09-981-353-127

Query Match	96.9%	Score 1315;	DB 9;	Length 250;
Best Local Similarity	98.4%	Pred. No. 1.1e-85;		
Matches 246;	Conservative	0;	Mismatches 0;	Indels 4;
Gaps	4;			
Qy	1	MADNFSLHDALSGGNPNPQGWPGANGNPAGAGGYPGASYPG-YPCQAPPGAYPGQAPP	59	
Db	1	MADNFSLHDALSGGNPNPQGWPGANGNPAGAGGYPGASYPGAYPGQAPPGAYPGQAPP	60	
Qy	60	GAYHGAPGAYPGAPAGVYPPGPGSGPGAYPSSQSPAGAY-ATGPGAPAGPLIYPYNL	118	
Db	61	GAYHGAPGAYPGAPAGVYPPGPGSGPGAYPSSQSPAGAYPATGPGAPAGPLIYPYNL	120	
Qy	119	PLPGGVVPRMLITILGTVKPNANRIALDFORGNDVAFHF-PRENENRRRIVIVCNKLDNN	177	
Db	121	PLPGGVVPRMLITILGTVKPNANRIALDFORGNDVAFHF-PRENENRRRIVIVCNKLDNN	180	
Qy	178	WGREERQSVPPFSGPKICVLVEPDHFKVAVNDAAH-LOYNHRVKKLNKLSIGSDI	236	
Db	181	WGREERQSVPPFSGPKFKIQVLVEPDHFKVAVNDAAHLLQYNHRVKKLNKLSIGSDI	240	

us-09-297-040-4.rapb

Tue May 20 14:40:26 2003

;; TITLE OF INVENTION: Galectin 8, 9, 10 and 10SV
;; NUMBER OF SEQUENCES: 60
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Sterne, Kessler, Goldstein, & Fox P.L.L.C.
;; STREET: 1100 New York Ave., Suite 600
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20005-3934
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/263,689
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/946,914
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Steffe, Eric K.
;; REGISTRATION NUMBER: 36,688
;; REFERENCE/DOCKET NUMBER: 1488.0560001/EKS/SGW
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 262 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-09-263-689-14

Query Match 79.5%; Score 1079; DB 10; Length 262;
Best Local Similarity 77.9%; Pred. No. 4.9e-69;
Matches 205; Conservative 16; Mismatches 24; Indels 18; Gaps 7;

QY 1 MADNFSLDALSGSNPNQPCWAGNPGAGGYPGAGYPSG--GQSPAGAY-ATGPY 105
DB 1 MADGFSLDALAGSNPNQPCWAGNQP--GAGGYGASYPGAYPGQAPPGYQAPP 59
QY 60 GAYHG-----APGAYGAPAGVYGPSPGAYPSS--GQSPAGAY-ATGPY 105
DB 60 SAYPGTGPSPAYPGTAPGAYPGTAPGAFPGQPGGAYPSAPGAYPATGPF 119
QY 106 GAPAGPLIVPNLPLPGGVPRMLITILGTVPKNANRIALDFQGNDAVAFHF-PRNENN 164
DB 120 GAPTGLTPVYDMLPGLGGVPRMLITILGTVPKNANSITLNFKNKGNDAIFHFPRNENN 179
QY 165 RRIVVNCNTKLDNNWGREERQSVFPESGPKFIQVLVEPDHFKVAVNDAAH-LOYNHRVKK 223
DB 180 RRIVVNCNTKLDNNWGREERQSVFPESGPKFIQVLVEADHFKVAVNDVHLLQYNHRMKN 239
QY 224 LNEISKLGISGDIIDLTASASYTMI 246
DB 240 LREISQLGIIGDITLTSASHAMI 262

RESULT 8
US-09-728-479-6
; Sequence 6, Application US/09728479
; Patent No. US20020034726A1
; GENERAL INFORMATION:
; APPLICANT: KANEGASAKI, SHIRO
; APPLICANT: MATSUMOTO, RYOJI
; APPLICANT: HIRASHIMA, MITSUOMI
; TITLE OF INVENTION: EOSINOPHIL CHEMOTACTIC FACTOR
; FILE REFERENCE: 3914-2
; CURRENT APPLICATION NUMBER: US/09/728,479

;; CURRENT FILING DATE: 2001-08-16
;; PRIOR APPLICATION NUMBER: PCT/JP99/02952
;; PRIOR FILING DATE: 1999-06-02
;; PRIOR APPLICATION NUMBER: JP 10/170698
;; PRIOR FILING DATE: 1998-06-02
;; NUMBER OF SEQ ID NOS: 12
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 6
;; LENGTH: 149
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; US-09-728-479-6

Query Match 55.4%; Score 752; DB 10; Length 149;
Best Local Similarity 98.6%; Pred. No. 3.1e-46;
Matches 146; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 101 ATGPYGAPAGPLIVPNLPLPGGVPRMLITILGTVPKNANRIALDFQGNDAVAFHF-PR 159
DB 2 ATGPYGAPAGPLIVPNLPLPGGVPRMLITILGTVPKNANRIALDFQGNDAVAFHFPR 61
QY 160 FNNRRRVIVCNTKLDNNWGREERQSVFPESGPKFIQVLVEPDHFKVAVNDAAH-LOYN 218
DB 62 FNNRRRVIVCNTKLDNNWGREERQSVFPESGPKFIQVLVEPDHFKVAVNDAAHLLQYN 121
QY 219 HRVKKLNEISKLGISGDIIDLTASASYTMI 246
DB 122 HRVKKLNEISKLGISGDIIDLTASASYTMI 149

RESULT 9
US-09-877-790-1
; Sequence 1, Application US/09877790
; Publication No. US20030054982A1
; GENERAL INFORMATION:
; APPLICANT: Jarvis, Gary
; APPLICANT: John, Constance
; APPLICANT: Leflier, Hakon
; TITLE OF INVENTION: N-TERMINALLY TRUNCATED GALECTIN-3 FOR USE IN TREATING CANCER
; FILE REFERENCE: 3157.00004
; CURRENT APPLICATION NUMBER: US/09/877,790
; CURRENT FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 143
; TYPE: PRT
; ORGANISM: homo sapien
; US-09-877-790-1

Query Match 53.3%; Score 723; DB 9; Length 143;
Best Local Similarity 98.6%; Pred. No. 3.3e-44;
Matches 141; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 106 GAPAGPLIVPNLPLPGGVPRMLITILGTVPKNANRIALDFQGNDAVAFHF-PRNENN 164
DB 1 GAPAGPLIVPNLPLPGGVPRMLITILGTVPKNANRIALDFQGNDAVAFHFPRNENN 60
QY 165 RRIVVNCNTKLDNNWGREERQSVFPESGPKFIQVLVEPDHFKVAVNDAAH-LOYNHRVKK 223
DB 61 RRIVVNCNTKLDNNWGREERQSVFPESGPKFIQVLVEPDHFKVAVNDAAHLLQYNHRVKK 120
QY 224 LNEISKLGISGDIIDLTASASYTMI 246
DB 121 LNEISKLGISGDIIDLTASASYTMI 143

RESULT 10
US-09-728-479-11
; Sequence 11, Application US/09728479
; Patent No. US20020034726A1
; GENERAL INFORMATION:
; APPLICANT: KANEGASAKI, SHIRO

APPLICANT: MATSUMOTO, RYOJI
APPLICANT: HIRASHIMA, MITSUOMI
TITLE OF INVENTION: EOSINOPHIL CHEMOTACTIC FACTOR
FILE REFERENCE: 3914-2
CURRENT APPLICATION NUMBER: US/09/728,479
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: PCF/JF99/02952
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: JP 10/170698
PRIOR FILING DATE: 1998-06-02
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 322
TYPE: PRT
ORGANISM: Mus sp.
US-09-728-479-11

Query Match 21.7%; Score 295; DB 10; Length 322;
Best Local Similarity 37.0%; Pred. No. 1.1e-13;
Matches 68; Conservative 29; Mismatches 47; Indels 40; Gaps 8;
QY 63 HGAPG---AYCAPAPGVYPPSGPAGYATGPGAPAGPLIYPYNLP 119
DB 168 HSTPGQMFSTGIP-PVYPTP-----AYT-----IPFYTP 197
QY 120 LPGVVVPRMLITILGTVKPNANRIALDFQGNDAVAFH-FRNNRRNVIVCTKLDNNW 178
DB 198 IENGLVPSKSMISLVLPDAREHINLRGCGDIAFHLPNREN---AVVRTQINNSW 254
QY 179 GREERQSV--PFESGKPFKIQVLVEPDHFKVAVNDAHL-QYNHRVKLNKLEISGDISD 235
DB 255 GOEERSLGRMPFVRGQSFVWICEGHCFKAVANGQHCYHRLKNLQDINTLEAVGD 314
QY 236 IDLT 239
DB 315 IQLT 318

RESULT 11
US-09-854-133-439
Sequence 439, Application US/09854133
Publication No. US20020183499A1
GENERAL INFORMATION:
APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Raodoh
APPLICANT: Henderson, Robert A.
APPLICANT: Benson, Darin R.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475C10
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 439
LENGTH: 378
TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-133-439

Query Match 21.3%; Score 289; DB 9; Length 378;
Best Local Similarity 36.2%; Pred. No. 3.5e-13;
Matches 75; Conservative 29; Mismatches 65; Indels 38; Gaps 9;
QY 66 PGAYPGAPA-----PGVYPPSGP-----PGAYPPSGQP-----SAPGAYAT 102
DB 173 PRTVPVQAFSAFVPSQPVCFPRGRQRKPPGVWPANPAPITQTVIHTVQSAPQMF 232
QY 103 GP-----YGAPAGPLIYPYNLPPLGGVVVPRMLITILGTVKPNANRIALDFQGNDAVAFH 156
DB 233 TPAIPPMYPHPAYPM--PFITITLGLVPSKILLSGTVLPSAQRHINLCSGNHIAPH 290

QY 157 F-PRFNNRRNVIVCTKLDNNWREERQ--SVFPFESGKPFKIQVLVEPDHFKVAVNDA 213
DB 291 LNPRFDE---AVVRTQIDNSGSEERSLPRKMPFVRGQSFVSWILCEAHCLKVAVDQG 347
QY 214 HL-QYNHRVKLNKLEISGDISDILT 239
DB 348 HLFYHYHRLNRLPTINRLEVGGDIQLT 374

RESULT 12
US-09-738-973-439
Sequence 439, Application US/09738973
Patent No. US20020110563A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Fling, Steven P.
APPLICANT: Mohamath, Raodoh
APPLICANT: Algata, Paul A.
APPLICANT: Secrist, Heather
APPLICANT: Indirias, Carol Ioseph
APPLICANT: Benson, Darin R.
APPLICANT: Elliot, Mark
APPLICANT: Mannion, Jane
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475C9
CURRENT APPLICATION NUMBER: US/09/738,973
CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 587
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 439
LENGTH: 378
TYPE: PRT
ORGANISM: Homo sapiens
US-09-738-973-439

Query Match 21.3%; Score 289; DB 10; Length 378;
Best Local Similarity 36.2%; Pred. No. 3.5e-13;
Matches 75; Conservative 29; Mismatches 65; Indels 38; Gaps 9;
QY 66 PGAYPGAPA-----PGVYPPSGP-----PGAYPPSGQP-----SAPGAYAT 102
DB 173 PRTVPVQAFSAFVPSQPVCFPRGRQRKPPGVWPANPAPITQTVIHTVQSAPQMF 232
QY 103 GP-----YGAPAGPLIYPYNLPPLGGVVVPRMLITILGTVKPNANRIALDFQGNDAVAFH 156
DB 233 TPAIPPMYPHPAYPM--PFITITLGLVPSKILLSGTVLPSAQRHINLCSGNHIAPH 290
QY 157 F-PRFNNRRNVIVCTKLDNNWREERQ--SVFPFESGKPFKIQVLVEPDHFKVAVNDA 213
DB 291 LNPRFDE---AVVRTQIDNSGSEERSLPRKMPFVRGQSFVSWILCEAHCLKVAVDQG 347
QY 214 HL-QYNHRVKLNKLEISGDISDILT 239
DB 348 HLFYHYHRLNRLPTINRLEVGGDIQLT 374

RESULT 13
US-09-728-479-2
Sequence 2, Application US/09728479
Patent No. US20020034726A1
GENERAL INFORMATION:
APPLICANT: KANEGASAKI, SHIRO
APPLICANT: MATSUMOTO, RYOJI
APPLICANT: HIRASHIMA, MITSUOMI
TITLE OF INVENTION: EOSINOPHIL CHEMOTACTIC FACTOR
FILE REFERENCE: 3914-2
CURRENT APPLICATION NUMBER: US/09/728,479
CURRENT FILING DATE: 2001-08-16

;; PRIOR APPLICATION NUMBER: PCT/JP99/02952
;; PRIOR FILING DATE: 1999-06-02
;; PRIOR APPLICATION NUMBER: JP 10/170698
;; PRIOR FILING DATE: 1998-06-02
;; NUMBER OF SEQ ID NOS: 12
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 2
;; LENGTH: 323
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-728-479-2

Query Match 20.9%; Score 283; DB 10; Length 323;
Best Local Similarity 34.1%; Pred. No. 7.9e-13;
Matches 73; Conservative 27; Mismatches 70; Indels 44; Gaps 8;
QY 38 GASYPGYPGQAPPAYPGQAPP-----GAYHGAPGAYPGAPA--PGVYPPSPGPGAYP 89
Db 138 GSVQLSYISFQPGVWPANPAPITQTVIHTVQSAPGQMFSTPAIPPMYPHP-----AYP 192
QY 90 SSGQPSAPGAYATGPGAPAGPLIVPNLPGVVPRLITILGTVKPNANRIALDQF 149
Db 193 -----MPFTITILGGLYPSKILLSGTVLPSAQRHINLCS 228
QY 150 GNDVAFHF--PRFNNRRVIVCNKLDNNGREERQ--SVFPFESGKPKIQVLVEPDHF 206
Db 229 GNHIAFHLNPRDEN---AVVRNTQIDNSWGSEERSLPRKMPFVRGQSFVWILCEAHCL 285
QY 207 KVAVND AHL-QYNHRVKKLNEISKLGISGDIDL 239
Db 286 KVAVDQHLFEYHRLNRLPTINRLEVGDIQLT 319

RESULT 14
US-09-728-479-12
;; Sequence 12, Application US/09728479
;; Patent No. US20020034726A1
;; GENERAL INFORMATION:
;; APPLICANT: KANEGASAKI, SHIRO
;; APPLICANT: MATSUMOTO, YOJI
;; APPLICANT: HIRASHIMA, MITSUOMI
;; TITLE OF INVENTION: EOSINOPHIL CHEMOTACTIC FACTOR
;; FILE REFERENCE: 3914-2
;; CURRENT APPLICATION NUMBER: US/09/728,479
;; CURRENT FILING DATE: 2001-08-16
;; PRIOR APPLICATION NUMBER: PCT/JP99/02952
;; PRIOR FILING DATE: 1999-06-02
;; PRIOR APPLICATION NUMBER: JP 10/170698
;; PRIOR FILING DATE: 1998-06-02
;; NUMBER OF SEQ ID NOS: 12
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 12
;; LENGTH: 323
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-728-479-12

Query Match 19.7%; Score 267; DB 10; Length 323;
Best Local Similarity 33.2%; Pred. No. 1.1e-11;
Matches 71; Conservative 27; Mismatches 72; Indels 44; Gaps 8;
QY 38 GASYPGYPGQAPPAYPGQAPP-----GAYHGAPGAYPGAPA--PGVYPPSPGPGAYP 89
Db 138 GSVQLSYISFQPGVWPANPAPITQTVIHTVQSAPGQMFSTPAIPPMYPHP-----AYP 192
QY 90 SSGQPSAPGAYATGPGAPAGPLIVPNLPGVVPRLITILGTVKPNANRIALDQF 149
Db 193 -----MPFTITILGGLYPSKILLSGTVLPSAQRHINLCS 228
QY 150 GNDVAFHF--PRFNNRRVIVCNKLDNNGREERQ--SVFPFESGKPKIQVLVEPDHF 206
Db 229 GNHIAFHLNPRDEN---AVVRNTQIDNSWGSEERSLPRKMPFVRGQSFVWILCEAHCL 285

QY 207 KVAVND AHL-QYNHRVKKLNEISKLGISGDIDL 239
Db 286 KVAVDQHLFEYHRLNRLPTINRLEVGDIQLT 319
RESULT 15
US-10-235-674-4
;; Sequence 4, Application US/10235674
;; Publication No. US20030040081A1
;; GENERAL INFORMATION:
;; APPLICANT: Ni, Jian
;; APPLICANT: Gentz, Reiner L.
;; APPLICANT: Ruben, Steven M.
;; TITLE OF INVENTION: Galectin 9 and 10SV Polynucleotides
;; FILE REFERENCE: 1488.0560004
;; CURRENT APPLICATION NUMBER: US/10/235,674
;; CURRENT FILING DATE: 2002-09-06
;; PRIOR APPLICATION NUMBER: US 09/656,450
;; PRIOR FILING DATE: 2000-09-06
;; PRIOR APPLICATION NUMBER: US 09/263,689
;; PRIOR FILING DATE: 1999-03-05
;; PRIOR APPLICATION NUMBER: US 08/946,914
;; PRIOR FILING DATE: 1997-10-09
;; PRIOR APPLICATION NUMBER: US 60/028,093
;; PRIOR FILING DATE: 1996-10-09
;; NUMBER OF SEQ ID NOS: 60
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 4
;; LENGTH: 311
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-235-674-4

Query Match 19.5%; Score 264; DB 9; Length 311;
Best Local Similarity 36.5%; Pred. No. 1.7e-11;
Matches 66; Conservative 25; Mismatches 52; Indels 38; Gaps 7;
QY 65 APGAYPGAPA--PGVYPPSPGPGAYPSSGQPSAPGAYATGPGAPAGPLIVPNLPLPG 122
Db 159 APQMFSTPAIPPMYPHP-----AYP-----MPFITILG 189
QY 123 GVVPRMLITILGTVKPNANRIALDQFGRNDVAFHF--PRFNNRRVIVCNKLDNNGRE 181
Db 190 GLYPSKILLSGTVLPSAQRHINLCSGNHIAFHLNPRDEN---AVVRNTQIDNSWGSE 246
QY 182 ERQ--SVFPFESGKPKIQVLVEPDHFKVAVND AHL-QYNHRVKKLNEISKLGISGDIDL 238
Db 247 ERSLEPRKMPFVRGQSFVWILCEAHCLKVAVDQHLFEYHRLNRLPTINRLEVGDIQ 306
QY 239 T 239
Db 307 T 307

Search completed: May 20, 2003, 12:21:04
Job time : 22 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 20, 2003, 12:17:35 ; Search time 20 Seconds
(without alignments)
1182.453 Million cell updates/sec

Title: US-09-297-040-4

Perfect score: 1357

Sequence: 1 MAONFSUHDALSGGNPNQ.....ISKLIGISGIDILFSASYMTI 246

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1.*

2: p1r2.*

3: p1r3.*

4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1315	96.9	250	2 A35820	galactin 3 - human
2	1082	79.7	264	2 A28651	galactose-specific
3	1082	79.7	264	2 A45983	lactose-binding le
4	1076.5	79.3	294	2 A49688	lactose-binding le
5	1075	79.2	262	2 A34889	IgE-binding protei
6	1049.5	77.3	245	2 A54909	carbohydrate-bind
7	1024	75.5	242	2 JC4300	galactin-3 - rabbi
8	437	32.2	139	2 S08576	lectin - mouse (fr
9	254	18.7	323	2 A55664	lectin L-36 - pig
10	250.5	18.5	145	2 A55932	galactin-5 - rat
11	236.5	17.4	324	2 A46631	lactose-binding le
12	223.5	16.5	317	2 JC6147	prostate carcinoma
13	218.5	16.1	316	2 A55975	galactin-8 - rat
14	211	15.5	136	2 I55469	galactin-7 - human
15	193	14.2	1049	1 CGB07S	collagen alpha 1(I
16	192.5	14.2	463	2 S29170	annexin VII - mous
17	180.5	14.0	177	2 S65780	glycine/proline-ri
18	189.5	14.0	329	2 T32783	hypothetical prote
19	188.5	13.9	279	2 T32716	beta-galactoside-b
20	188.5	13.9	285	2 T26325	hypothetical prote
21	188	13.9	744	2 S15435	collagen alpha 1(V
22	187.5	13.8	313	2 T22828	hypothetical prote
23	186.5	13.7	179	2 A85217	hypothetical prote
24	186.5	13.7	277	2 T04441	hypothetical prote
25	186	13.7	488	1 LUH07	annexin VII, long
26	185.5	13.7	488	2 A27353	collagen alpha 1(I
27	184	13.6	299	2 T19564	hypothetical prote
28	183.5	13.5	743	1 S23779	collagen alpha 1(V
29	183	13.5	299	2 T25407	hypothetical prote

ALIGNMENTS

RESULT 1

A35820

Galactin 3 - human

N:Alternate names: CBP 35; epithelial-specific lectin 35; galactoside-binding lectin
C:Species: Homo sapiens (man)
C:Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 20-Apr-2000
C:Accession: A35820; JQ0916; A47473; A36071; A49800
R:Robertson, M.W.; Albrandt, K.; Keller, D.; Liu, F.T.
Biochemistry 29, 8093-8100, 1990

A:Title: Human IgE-binding protein: a soluble lectin exhibiting a highly conserved in
A:Reference number: A35820; MUID:91084480; PMID:2261464
A:Accession: A35820

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-250 <ROB>

A:Cross-references: GB:M57710; MID:g179530; PIDN:AAA35607.1; PID:g179531; GB:J02921
R:Oda, Y.; Leffler, H.; Sakakura, Y.; Kasai, K.; Barondes, S.H.
Gene 99, 279-283, 1991

A:Title: Human breast carcinoma cDNA encoding a galactoside-binding lectin homologous
A:Reference number: JQ0916; MUID:91216471; PMID:3022338

A:Accession: JQ0916

A:Molecule type: mRNA

A:Residues: 1-250 <ODA>

A:Cross-references: GB:M36682; MID:g186921; PIDN:AAA36163.1; PID:g186922
R:Lotz, M.M.; Andrews Jr., C.W.; Korzeilius, C.A.; Lee, E.C.; Steele Jr., G.D.; Clarke
Proc. Natl. Acad. Sci. U.S.A. 90, 3466-3470, 1993

A:Title: Decreased expression of Mac-2 (carbohydrate binding protein 35) and loss of
A:Reference number: A47473; MUID:93234518; PMID:7682704

A:Accession: A47473

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-63, 'P', '55-97', 'N', '99-250 <LOT>

A:Cross-references: GB:SS5012; MID:g299601; PIDN:AAB26229.1; PID:g299602

A:Experimental source: normal colonic mucosa, colon carcinoma, cell line clone A

A:Note: sequence extracted from NCBI backbone (NCBIN:129689, NCBI:129692)

R:Cherayil, B.J.; Chaitovitz, S.; Wong, C.; Pillai, S.

Proc. Natl. Acad. Sci. U.S.A. 87, 7324-7328, 1990

A:Title: Molecular cloning of a human macrophage lectin specific for galactose.

A:Reference number: A36071; MUID:90384999; PMID:2402511

A:Accession: A36071

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-32, 'O', '34', 'L', '37', 'RGFLSWGL', '46', 'RAGT', '51', 'R', '53-63', 'P', '65-87, 89-250 <CH

A:Cross-references: GB:M35368; MID:g1196441

A:Note: the sequence is revised in GenBank entry HUMMAC2, release 113.0, PIDN:AAA8808

R:Kaz, A.; Carmi, P.; Raz, T.; Hogan, V.; Mohamed, A.; Wolman, S.R.

Cancer Res. 51, 2173-2178, 1991

A:Title: Molecular cloning and chromosomal mapping of a human galactoside-binding pro

A:Reference number: A49800; MUID:91183475; PMID:2009535

A:Accession: A49800

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

Tue May 20 14:40:26 2003

A:Residues: 1-32, 'Q', 34, 'LPAGSYGAYGAGTPTCLSWTAPPATMEHVELIRSTCTWSLRTQ', 86-104, 'A', 106, 'M'
A:Cross-references: GB:M64303; NID:9413862
A:Note: this translation is not annotated in GenBank entry HUMGALBIN, release 113.0
C:Genetics:
A:Gene: GDB:LGALS3; MAC-2; LGALS2
A:Cross-references: GDB:127515; OMIM:137033
A:Map position: lp13-lp13
C:Superfamily: beta-galactoside-binding lectin
C:Keywords: lectin; nucleus; phosphoprotein

Query Match 96.9%; Score 1315; DB 2; Length 250;
Best Local Similarity 98.4%; Pred. No. 9.5e-85;
Matches 246; Conservative 0; Mismatches 0; Indels 4; Gaps 4;

QY 1 MADNFSLDALSGSGNPNPQGWPGAGNQPAGAGYPGASYPG-YPGQAPPYPGQAPP 59
DB 1 MADNFSLDALSGSGNPNPQGWPGAGNQPAGAGYPGASYPG-YPGQAPPYPGQAPP 60
QY 60 GAYGAPGAPGAPGAYPGGPPSGGAYPSSGQPSAPGAY-ATGPGYAGAPGLIYVYNL 118
DB 61 GAYGAPGAPGAPGAYPGGPPSGGAYPSSGQPSAPGAY-ATGPGYAGAPGLIYVYNL 120
QY 119 PLPGGVPRMLITILGTVPKPNANRIALDFQRNDVAFHF-PRFNNRRVIVCNKLDNN 177
DB 121 PLPGGVPRMLITILGTVPKPNANRIALDFQRNDVAFHF-PRFNNRRVIVCNKLDNN 180
QY 178 WGRERQSVFFESGKPKIOVLVEPDHFKVAVNDAH-LOYNHVRVKLNKLSIGSDI 236
DB 181 WGRERQSVFFESGKPKIOVLVEPDHFKVAVNDAH-LOYNHVRVKLNKLSIGSDI 240
QY 237 DLTSASYTMI 246
DB 241 DLTSASYTMI 250

RESULT 2
A28651
galactose-specific lectin - mouse
N:Alternate names: carbohydrate-binding protein 35; IgE-binding protein; lectin L-34; Ma
C:Species: Mus musculus (house mouse)
C:Date: 28-Aug-1989 #sequence_revision 10-Feb-1995 #text_change 20-Aug-1999
A:Accession: S08537; A28651; A37385; A35185
R:Cherayil, B.J.; Weiner, S.J.; Pillai, S.
J. Exp. Med. 170, 1959-1972, 1989
A:Title: The Mac-2 antigen is a galactose-specific lectin that binds IgE.
A:Reference number: S08537; MUID:90063462; PMID:2584931
A:Accession: S08537
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-264 <CHE>
A:Cross-references: EMBL:X16834; NID:952986; PIDN:CAA34736.1; PID:952987
A:Note: this sequence was submitted to the EMBL Data Library, Oct-1989
R:Jia, S.; Wang, J.L. 6009-6011, 1988
J. Biol. Chem. 263, 6009-6011, 1988
A:Title: Carbohydrate binding protein 35. Complementary DNA sequence reveals homology w
A:Reference number: A28651; MUID:88198129; PMID:3360772
A:Accession: A28651
A:Molecule type: mRNA
A:Residues: 'R', 3-264 <JIA>
R:Cross-references: EMBL:J03723
R:Raz, A.; Pazerini, G.; Carmi, P.
Cancer Res. 49, 3489-3493, 1989
A:Title: Identification of the metastasis-associated, galactoside-binding lectin as a ch
A:Reference number: A37385; MUID:89275058; PMID:2525069
A:Accession: A37385
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-3, 'T', 5-91, 'ST', 94-109, 'SAP', 113-264 <RAZ>
A:Cross-references: GB:X16074; NID:952850; PIDN:CAA34206.1; PID:952851
A:Note: authors translated the codon GAA for residue 219 as Ala, GAC for residue 221 as
R:Woo, H.J.; Shaw, L.M.; Messler, J.M.; Mercurio, A.M.
J. Biol. Chem. 265, 7097-7099, 1990
A:Title: The major non-integrin laminin binding protein of macrophages is identical to d

A:Reference number: A35185; MUID:90236991; PMID:2332426
A:Accession: A35185
A:Molecule type: Protein
A:Residues: 159-163; 166-175; 214-226 <WOO>
C:Superfamily: beta-galactoside-binding lectin
C:Keywords: lectin; phosphoprotein

Query Match 79.7%; Score 1082; DB 2; Length 264;
Best Local Similarity 78.0%; Pred. No. 1.7e-68;
Matches 209; Conservative 16; Mismatches 17; Indels 26; Gaps 8;

QY 1 MADNFSLDALSGSGNPNPQGWPGAGNQPAGAGYPGASYPG-YPGQAPPYPGQAPP 59
DB 1 MADNFSLDALSGSGNPNPQGWPGAGNQPAGAGYPGASYPG-YPGQAPPYPGQAPP 59
QY 60 GAYHG-----APGAYGAPGAPGAYPGGPPSGGAYPSSGQPSAPGAY----- 100
DB 60 GAYHG-----APGAYGAPGAPGAYPGGPPSGGAYPSSGQPSAPGAY----- 116
QY 101 ATGPGYAGAPGLIYVYNLPLPGGVPRMLITILGTVPKPNANRIALDFQRNDVAFHF-PR 159
DB 117 AAGPYGAPGLIYVYNLPLPGGVPRMLITILGTVPKPNANRIALDFQRNDVAFHF-PR 176
QY 160 FNNRRVIVCNKLDNNWGRERQSVFFESGKPKIOVLVEPDHFKVAVNDAH-LOYN 218
DB 177 FNNRRVIVCNKLDNNWGRERQSVFFESGKPKIOVLVEPDHFKVAVNDAH-LOYN 236
QY 219 HRVKLNKLSIGSDIDITLSASYTMI 246
DB 237 HRVKLNKLSIGSDIDITLSASYTMI 264

RESULT 3
A45983
lactose-binding lectin Mac-2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 03-May-1996
R:Rosenberg, I.M.; Iyer, R.; Cherayil, B.; Chiodino, C.; Pillai, S.
J. Biol. Chem. 268, 12393-12400, 1993
A:Title: Structure of the murine Mac-2 gene. Splice variants encode proteins lacking
A:Reference number: A45983; MUID:93286070; PMID:8509379
A:Accession: A45983
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-264 <ROS>
A:Cross-references: GB:I08649
C:Genetics:
A:Introns: 6/3; 128/3; 158/2; 209/2; 213/3
C:Superfamily: beta-galactoside-binding lectin

Query Match 79.7%; Score 1082; DB 2; Length 264;
Best Local Similarity 78.6%; Pred. No. 1.7e-68;
Matches 209; Conservative 15; Mismatches 20; Indels 22; Gaps 8;

QY 1 MADNFSLDALSGSGNPNPQGWPGAGNQPAGAGYPGASYPG-YPGQAPPYPGQAPP 59
DB 1 MADNFSLDALSGSGNPNPQGWPGAGNQPAGAGYPGASYPG-YPGQAPPYPGQAPP 59
QY 60 GAYHG--APGAYGAPGAPGAYPGGPPSGGAYPSS-----GQPSAPGAY-----AT 102
DB 60 GAYHG--APGAYGAPGAPGAYPGGPPSGGAYPSS-----GQPSAPGAY----- 118
QY 103 GPGYAGAPGLIYVYNLPLPGGVPRMLITILGTVPKPNANRIALDFQRNDVAFHF-PRFN 161
DB 119 GPGYAGAPGLIYVYNLPLPGGVPRMLITILGTVPKPNANRIALDFQRNDVAFHF-PRFN 178
QY 162 ENNRRVIVCNKLDNNWGRERQSVFFESGKPKIOVLVEPDHFKVAVNDAH-LOYNHR 220
DB 179 ENNRRVIVCNKLDNNWGRERQSVFFESGKPKIOVLVEPDHFKVAVNDAH-LOYNHR 238
QY 221 VKLNKLSIGSDIDITLSASYTMI 246
DB 237 VKLNKLSIGSDIDITLSASYTMI 264

Db 239 MNLRISQIGSDITLTSANAMI 264

RESULT 4

A49688
lactose-binding lectin L-29 - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 24-Nov-1999
C:Accession: A49688
J:Herzmann, J.; Turk, C.W.; Atchison, R.E.; Huflejt, M.E.; Poulter, L.; Gitt, M.A.; Bur
J. Biol. Chem. 268, 26704-26711, 1993
A:Title: Primary structure of the soluble lactose binding lectin L-29 from rat and dog a
genase.

A:Reference number: A49688; MUID:94073368; PMID:8253805

A:Accession: A49688

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-294 <HER>

A:Cross-references: GB:L23429

C:Superfamily: beta-galactoside-binding lectin

C:Keywords: acetylated amino end

F:1/Modified site: acetylated amino end (Ala) #status experimental

Query Match 79.3%; Score 1076.5; DB 2; Length 294;

Best Local Similarity 70.8%; Pred. No. 4.6e-68;

Matches 209; Conservative 13; Mismatches 22; Indels 51; Gaps 7;

QY 2 ADNFSLDALSGSNPNPQGWPGANGNPAGAGGYPGASYP----- 42

DB 1 ADSFSLNDA-SGSGNPNPQGWPGANGNPAGAGGYPGASYPGAYPGQAPPGYPGQAPPG 59

QY 43 -----GYPGQAPPGAYPGQAPPGAYHG--APGAYGAPAPGYVPGP----- 81

DB 60 GYPGQAPPGYPGQAPPGYVPGQAPPGYVPGQAPPGYVPGQAPPGYVPGQAPPGYVPGPTA 119

QY 82 -----PSGCAYPSSGOPSAPGAY-ATGPYCAPAGLIVPNLPLPGGVPRMLITIL 133

DB 120 PGTQPGSGGAYPPGOPSAPGAYPAAGPGIGAPGLTVPYDPLPLPGGVPRMLITIL 179

QY 134 GTVKPNANRIALDFQGNDAVAFHF--PRENENRRVIVCTKLDNNGREERQSVFPFESG 192

DB 180 GTVRESNRLALDFRGNDVAFHFENPRENEDNKRIVCTKLDNNGREERQSVFPFESG 239

QY 193 KPFKIQVLVEPDHFVKVANDAH-LOYNHRVKKLNEISKIGISGIDILTSASYTMI 246

DB 240 KPFKIQVLVESDHFVKVANDAHLLQYNHRMKNLPEISKIGISGIDILTSASYAMI 294

RESULT 5

A54889
IgE-binding protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 04-Nov-1994 #sequence_revision 04-Nov-1994 #text_change 20-Aug-1999
C:Accession: A54889; A23148
R:Albrandt, K.; Orida, N.K.; Liu, F.T.
Proc. Natl. Acad. Sci. U.S.A. 84, 6859-6863, 1987
A:Title: An IgE-binding protein with a distinctive repetitive sequence and homology with
A:Reference number: A54889; MUID:88016189; PMID:2958848
A:Accession: A54889
A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-262 <ALB>

A:Cross-references: GB:J02962; NID:g203173; PIDN:AAA40828.1; PID:g203174

R:Liu, F.T.; Albrandt, K.; Mendel, E.; Kulczycki Jr., A.; Orida, N.K.

Proc. Natl. Acad. Sci. U.S.A. 82, 4100-4104, 1985

A:Title: Identification of an IgE-binding protein by molecular cloning.

A:Reference number: A23148; MUID:85216041; PMID:3858867

A:Accession: A23148

A:Molecule type: mRNA

A:Residues: 125-262 <LIU>

A:Cross-references: GB:M13697; NID:g204727; PIDN:AAA41378.1; PID:g204728

C:Superfamily: beta-galactoside-binding lectin

C:Keywords: lectin; phosphoprotein

Query Match

Best Local Similarity 77.6%; Score 1075; DB 2; Length 262;

Matches 204; Conservative 17; Mismatches 24; Indels 18; Gaps 7;

QY 1 MADNFSLDALSGSNPNPQGWPGANGNPAGAGGYPGASYPG-YFGQAPPGAYPGQAPP 59

DB 1 MADGFSLDALAGSGNPNPQGWPGANGNP-GAGGYPGASYPGAYPGQAPPGYPGQAPP 59

QY 60 GAYHG-----APGAYGAPAPGYVPGPPSGPGAYPSS--GOPSAPGAY-ATGPY 105

DB 60 SAYPGTGSAYPGTAPGAYPGTAPGAFPGQPGGPGAYPSAPGAYPSAPGAYPATGP 119

QY 106 GAPAGLIVPNLPLPGGVPRMLITILGTVPKNANRIALDFQGNDAVAFHF--PRENENN 164

DB 120 GAPTGLTVPYDMLPGGVPRMLITILGTVPKNANSITLNFKKGNDAVAFHFNPRENENN 179

QY 165 RRVIVCTKLDNNGREERQSVFPFESGPFKIQVLVEPDHFVKVANDAH-LOYNHRVKK 223

DB 180 RRVIVCTKLDNNGREERQSVFPFESGPFKIQVLVEADHFVKVANDVHLLQYNHRMKN 239

QY 224 LNEISKIGISGIDILTSASYTMI 246

DB 240 LREISQIGIIGDITLTSASHAMI 262

RESULT 6

A54909

carbohydrate-binding protein CBP30 - hamster

N:Alternate names: S-type animal lectin CBP30

C:Species: Cricetinae gen. sp. (hamster)

C:Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 20-Aug-1999

C:Accession: A54909

R:Meul, B.; Bawumla, S.; Martin, S.R.; Hughes, R.C.

J. Biol. Chem. 269, 18250-18258, 1994

A:Title: Structure of baby hamster kidney carbohydrate-binding protein CBP30, an S-ty

A:Reference number: A54909; MUID:94299346; PMID:8027086

A:Accession: A54909

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-245 <MEH>

A:Cross-references: GB:X78879; NID:g535082; PIDN:CAA55479.1; PID:g535083

C:Superfamily: beta-galactoside-binding lectin

C:Keywords: lectin

Query Match

Best Local Similarity 81.0%; Score 1049.5; DB 2; Length 245;

Matches 204; Conservative 12; Mismatches 23; Indels 13; Gaps 8;

QY 1 MADNFSLDALSGSNPNPQGWPGANGNPAGAGGYPGASYPG-YFGQAPPGAYPGQAPP 59

DB 1 MADGFSLDALAGSGNPNPQGWPGANGNP-GAGGYPGASYPGAYPGQAPPGYPGQAPP 59

QY 60 GAYHG--APGAYGAPAPGYVPGPPSGPGAYPSSGOPSAPGAY-ATGPYCAPAGLIVPY 116

DB 60 GAYPGTAPGAYPG-PAPGAYPGQPGASGAY-----PSAPGAYPAAGPYGAPTALTVPY 113

QY 117 NLPLPGGVPRMLITILGTVPKNANRIALDFQGNDAVAFHF--PRENENRRVIVCTKLD 175

DB 114 KLPLAGGVPRMLITILGTVPKNANRIILNLRGNDIAHFHFNPRENENRRVIVCTKLD 173

QY 176 NNGREERQSVFPFESGPFKIQVLVEPDHFVKVANDAH-LOYNHRVKKLNEISKIGISG 234

DB 174 NNGREERQSVFPFESGPFKIQVLVEADHFVKVANDAHLLQYNHRMKNLREINQMEISG 233

QY 235 DIDLTSASYTMI 246

DB 234 DITLTSAPATMI 245

RESULT 7

JC4300

galectin-3 - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 20-Aug-1999
C:Accession: J04300
R:Gaudin, J.C.; Monsigny, M.; Legrand, A.
Gene 163, 249-252, 1995
A:Title: Cloning of the cDNA encoding rabbit galectin-3.
A:Reference number: J04300; MUID:96011642; PMID:7590275
A:Accession: J04300
A:Molecule type: mRNA
A:Residues: 1-242 <GAD>
A:Cross-references: GB:006470; NID:9606794; PIDN:AAC48491.1; PID:9606795
A:Experimental source: vascular smooth muscle cells
A:Note: The authors translated the codon TGC for residue 155 as Leu
C:Comment: This protein has the functions on cell adhesion and proliferation. It is a su
C:Genetics:
A:Gene: Igals3
C:Superfamily: beta-galactoside-binding lectin
C:Keywords: muscle

Query Match 75.5% Score 1024; DB 2; Length 242;
Best Local Similarity 78.8%; Pred. No. 1.7e-64;
Matches 197; Conservative 15; Mismatches 26; Indels 12; Gaps 7;
QY 1 MADNFSLDLSSGNPNQPGWAGNQFAGAGGYPGCAAYPG-YPGAPPGAYPGQAPP 59
DB 1 MADGFSLDLSSGSHPPNQPGWAGNQFAGAGGYPGCAAYPG-YPGAPPGAYPGQAPP 59
QY 60 GAYGAPGAYPGAPGAYPGGPGGAYPSSGQPSAPGAY-ATGPGYAGAPGLIVPVN 118
DB 60 GPYPG-PCGA-----GAYPGGPGGAYPSSGQPSAPGAY-ATGPGYAGAPGLIVPVN 112
QY 119 PLPGGVVPRMLITILGTVPKPNANRIALDFORGNDAVAFH-PRFNENRRVIVCTKLDNN 177
DB 113 PLPGGVVPRMLITILGTVPKPNANRIALDFORGNDAVAFH-PRFNENRRVIVCTKLDNN 172
QY 178 WGREERQVTFPEIGKPKFQVLEPDPHFKAIVNDAH-LQVNRHVKKLNKISGLIGSDI 236
DB 173 WGREERQVTFPEIGKPKFQVLEPDPHFKAIVNDAH-LQVNRHVKKLNKISGLIGSDI 232
QY 237 DLTSASYTWI 246
DB 233 QLTSAHAM 242

RESULT 8
S08576
lectin - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
C:Accession: S08576
R:Raz, A.; Carmi, P.; Pazerini, G.
Cancer Res. 48, 645-649, 1988
A:Title: Expression of two different endogenous galactoside-binding lectins sharing sequ
A:Reference number: S07162; MUID:88080093; PMID:3335026
A:Accession: S08576
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-139 <RAZ>
C:Superfamily: beta-galactoside-binding lectin

Query Match 32.2% Score 437; DB 2; Length 139;
Best Local Similarity 75.9%; Pred. No. 7.2e-24;
Matches 85; Conservative 6; Mismatches 19; Indels 2; Gaps 2;
QY 104 PYGAPAGPLIVPVNPLPGGVVPRMLITILGTVPKPNANRIALDFORGNDAVAFH-PRFNE 162
DB 22 PLWCPRWTVDVDFDLPLPGGVVPRMLITILGTVPKPNANRIALDFORGNDAVAFH-PRFNE 81
QY 163 NNRNVIVCTNKLNNWGREERQSVFFESGKPKFQVLEPDPHFKAIVNDAH 214
DB 82 NNRNVIVCTNKLNNWGREERQSVFFESGKPKFQVLEPDPHFKAIVNDAH 132

RESULT 9
A55664
lectin L-36 - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 29-Sep-1999
C:Accession: A55664
R:Chiu, M.L.; Parry, D.A.D.; Feldman, S.R.; Klapper, D.G.; O'Keefe, E.J.
J. Biol. Chem. 269, 31770-31776, 1994
A:Title: An adherens junction protein is a member of the family of lactose-binding le
A:Reference number: A55664; MUID:95081129; PMID:7989350
A:Accession: A55664
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-323 <CHI>
A:Cross-references: GB:X79303; NID:9623345; PIDN:CAA55884.1; PID:9623346
C:Superfamily: lactose-binding lectin L-36

Query Match 18.7% Score 254; DB 2; Length 323;
Best Local Similarity 37.6%; Pred. No. 9.8e-11;
Matches 68; Conservative 22; Mismatches 77; Indels 14; Gaps 8;
QY 71 GAPAGVYPPGPPSGPGAYPSSGQPSAPGAYATGPGYAGAPGLIVPVNPLPGGVVPRMLI 130
DB 152 GQAPS--PGMPNPG-YPGPKHNOQPCNLPCMECAPTFNPVPYKTRLOGLVARRTI 208
QY 131 TILGTVPKPNANRIALDFORGN--DVAFH-PRFNENRRVIVCTNKLNNWGREERQSVF 187
DB 209 VIKGYVPPSGKSLVINFKVSGSDVALHINPRLTEG---IVVRNSYINGKWAERKSSF 265
QY 188 -PFESGKPKFQVLEPDPHFKAIVNDAH-LQVNRHVKKLNKISGLIGSDI 245
DB 266 NPFAPQYFDLSIRCGLDLRFKRYANGHOLFDFSHRUSNFCQGVDTLEIQGVDTL---SYVQ 322
QY 246 I 246
DB 323 I 323

RESULT 10
A55932
galectin-5 - rat
N:Alternate names: beta-galactoside binding lectin
C:Species: Rattus norvegicus (Norway rat)
C:Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 21-Jan-2000
C:Accession: A55932; PX0077
R:Gitt, M.A.; Wiser, M.F.; Leffler, H.; Herrmann, J.; Xia, Y.R.; Massa, S.M.; Cooper,
J. Biol. Chem. 270, 5032-5038, 1995
A:Title: Sequence and mapping of galectin-5, a beta-galactoside-binding lectin, found
A:Reference number: A55932; MUID:95197487; PMID:7890611
A:Accession: A55932
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-145 <GIT>
A:Cross-references: GB:I36862; NID:9727175; PIDN:AAC42050.1; PID:9727176
R:Jung, S.K.; Fujimoto, D.
J. Biochem. 116, 547-553, 1994
A:Title: A novel beta-galactoside-binding lectin in adult rat kidney.
A:Reference number: PX0077; MUID:95155264; PMID:7852273
A:Accession: PX0077
A:Molecule type: protein
A:Residues: 7, 'p', 9-10, 'T', 12-19, 'X', 21-25, 30-42, 109-111, 'N', 113, 'H', 115, 'VS', 118-123
A:Experimental source: kidney
C:Comment: This protein exhibits activity to various saccharides and binds to Engelbr
C:Genetics:
A:Gene: LGALS5
C:Superfamily: beta-galactoside-binding lectin
C:Keywords: acetylated amino end; lectin; monomer
F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental

Query Match 18.5% Score 250.5; DB 2; Length 145;
Best Local Similarity 40.4%; Pred. No. 7.3e-11;
Matches 55; Conservative 26; Mismatches 48; Indels 7; Gaps 4;

[illegible]

A; Cross-references: GB:L07769; NID:g182131; PIDN:AAA67899.1; PID:g1821332
C:Genetics:
A:Gene: GDB:LGALS7
A; Cross-references: GDB:578907; OMIM:600615
A; Map position: 19pter-19qter
C:Superfamily: beta-galactoside-binding lectin

Query Match	15.5%	Score 211;	DB 2;	Length 136;
Best Local Similarity Matches	35.3%;	Pred. No.	3.8e-08;	
Matches	47;	Conservative	28;	Mismatches 48; Indels 10; Gaps
Qy	114	VPNYLPGGGVPRMLTITILGTVPKANRTALDF---	QEGNDVAFHF-PFRFNENRRVI	168
Dd	4	VPHKSLPEGIRGVTGURIGLVPPNASHFHVLLCGE	QSGDAUHFNPRLDTSE---V	60
Qy	169	VCNTIKLDNNRGRERQSVFFPGSKPFKIQLVLP	HOFHKVAVNDA-HLQYNHRVKKLNEI	227
Dd	61	VFNSKEGSGNGREGRGPVFQRQPPEVLIIASDD	GFKAVVGDAQYHHFHRL-PLARV	119
Qy	228	SKLGISGDILT	S 240	
Dd	120	RLVEVGGDVOLD	S 132	

RESULT 15

CG807S
collagen alpha 1(III) chain - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 07-May-1999
C:Accession: A02862; A38001; A38002; A38003; A38004; A38005; S71946
R:Fietzek, P.P.; Allmann, H.; Rautenberg, J.; Henkel, W.; Wachter, E.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 809-820, 1979
A:Title: The covalent structure of calf skin type III collagen. I. The amino acid sequence of the alpha 1(III) chain
A:Reference number: A02862; MUID:80026026; PMID:488906
A:Accession: A02862
A:Molecule type: protein
A:Residues: 1-242 <FIE>
R:Dewes, H.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 821-832, 1979
A:Title: The covalent structure of calf skin type III collagen. II. The amino acid sequence of the alpha 2(I) chain
A:Reference number: A38001; MUID:80026027; PMID:488907
A:Accession: A38001
A:Molecule type: protein
A:Residues: 243-422 <DEW1>
R:Bentz, H.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 833-840, 1979
A:Title: The covalent structure of calf skin type III collagen. III. The amino acid sequence of the alpha 1(I) chain
A:Reference number: A38002; MUID:80026028; PMID:488908
A:Accession: A38002
A:Molecule type: protein
A:Residues: 423-571 <BEN>
R:Lang, H.; Glangville, R.W.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 841-850, 1979
A:Title: The covalent structure of calf skin type III collagen. IV. The amino acid sequence of the alpha 2(II) chain
A:Reference number: A38003; MUID:80026029; PMID:488909
A:Accession: A38003
A:Molecule type: protein
A:Residues: 572-808 <LAN>
R:Dewes, H.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 851-860, 1979
A:Title: The covalent structure of calf skin type III collagen. V. The amino acid sequence of the alpha 1(II) chain
A:Reference number: A38004; MUID:80026030; PMID:488910
A:Accession: A38004
A:Molecule type: protein
A:Residues: 809-947 <DEW2>
R:Allmann, H.; Fietzek, P.P.; Glangville, R.W.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 861-868, 1979
A:Title: The covalent structure of calf skin type III collagen. VI. The amino acid sequence of the alpha 2(I) chain
A:Reference number: A38005; MUID:80026031; PMID:488911
A:Accession: A38005
A:Molecule type: protein
A:Residues: 948-1049 <ALL>
A:Experimental source: skin

R;Henkel, W. Biochem. J. 318, 497-503, 1996
A;Title: Cross-link analysis of the C-telopeptide domain from type III collagen.
A;Reference number: S71946; MUID:96404897; PMID:8809038
A;Accession: S71946
A;Molecule type: protein
A;Residues: 87-106;1017-1029;1037-1049 <HENS>
C;Comment: Prolines at the third position of the tripeptide repeating unit (G-X-Y) ar
C;Comment: The type III collagen molecule is a trimer of identical chains, linked to
C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homolo
C;Keywords: coiled coil; extracellular matrix; glycoprotein; hydroxyllysine; hydroxypr
F:1-1049/Product: collagen alpha 1(III) chain #status experimental <CAB>
F:1-14/Region: amino-terminal nonhelical telopeptide
F:15-1040/Region: helical
F:157-589/Region: cell attachment (R-G-D) motif
F:752-754/Region: cell attachment (R-G-D) motif
F:875-877/Region: cell attachment (R-G-D) motif
F:878-880/Region: cell attachment (R-G-D) motif
F:935-937/Region: cell attachment (R-G-D) motif
F:1041-1049/Region: carboxyl-terminal nonhelical telopeptide
F:95,107,119,938,950/Modified site: 5-hydroxyllysine (lys) #status experimental
F:107,950/Modified site: allysine (lys) #status predicted
F:107/Binding site: carbohydrate (lys) (covalent) #status experimental
F:1040,1041/Disulfide bonds: interchain #status predicted

Query Match	14.2%;	Score 193;	DB 1;	Length 1049;
Best Local Similarity	33.7%;	Pred. No. 6.le-06;		
Matches	64;	Conservative	8;	Mismatches 58; Indels 60; Gaps
Qy	5	FSLHDLSG-----SNCNPNQGWPGAWGNQAGAGYPCGASYPGYG-QAPPAPGPQA	57	
Dd	2	YEADVRSVAGNGIAGYCPGAPGGPPG--PPTSGHPCA--PGAPGVQGPGE-PGA	56	
Qy	58	PPGAYHGACPAY-----PGAPAGVPYPPPP--SQPGAYP-----	89	
Dd	57	GPAGPPPPGAIGSPGKDGSRRGRPRGFRFPCKMGKPGACMPGPFPMKGHRGDFGRN	116	
Qy	90	-SSGQPSAAGAY----ATGPYGAPA--GPLIVYNPLPGVVYPRMLITLTGTVKFNANR	142	
Dd	117	GKGEQAGAPLKGENVGEDGAPCMGRPACGERGRPG-----LPGAAGARGN-	166	
Qy	143	IALDFQRGND	152	
Dd	167	--DGARSD	173	

Search completed: May 20, 2003, 12:20:00
Job time : 22 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 20, 2003, 12:15:10 ; Search time 11 Seconds
(without alignments)
927.562 Million cell updates/sec

Title: US-09-297-040-4

Perfect score: 1357

Sequence: 1 MADNFSLHLDLSSGNNPNQ.....ISKLGISGIDILTSASYTMI 246

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1310	96.5	249	1	LEG3_HUMAN
2	1091	80.4	295	1	LEG3_CANFA
3	1077	79.4	263	1	LEG3_MOUSE
4	1074	79.1	261	1	LEG3_RAT
5	1044.5	77.0	244	1	LEG3_CRILLO
6	1019	75.1	241	1	LEG3_RABIT
7	299	22.0	353	1	LEG9_MOUSE
8	289	21.3	355	1	LEG9_HUMAN
9	276.5	20.4	354	1	LEG9_RAT
10	254	18.7	323	1	LEG4_PIG
11	250.5	18.5	144	1	LEG5_RAT
12	245	18.1	301	1	LEG6_MOUSE
13	236.5	17.4	324	1	LEG4_RAT
14	228.5	16.8	316	1	LEG8_HUMAN
15	218.5	16.1	316	1	LEG8_RAT
16	215.5	15.9	323	1	LEG4_HUMAN
17	211	15.5	135	1	LEG7_HUMAN
18	207.5	15.3	316	1	LEG8_MOUSE
19	196.5	14.5	466	1	ANK7_HUMAN
20	193	14.2	1049	1	CA13_BOVIN
21	192.5	14.2	463	1	ANK7_MOUSE
22	188.5	13.9	279	1	LE32_CAEEL
23	188	13.9	467	1	CBPA_DICDI
24	187.5	13.8	283	1	LEG1_HAECO
25	187	13.8	684	1	CA39_HUMAN
26	185	13.6	744	1	CA18_HUMAN
27	184	13.6	135	1	LEG7_RAT
28	183.5	13.5	743	1	CA18_MOUSE
29	181	13.3	336	1	LEG8_HUMAN
30	180	13.3	744	1	CA18_RABIT
31	179	13.2	316	1	CC12_CAEEL
32	179	13.2	316	1	CC13_CAEEL
33	174.5	12.9	296	1	CC01_CAEEL

RESULT 1

ID	LEG3_HUMAN	STANDARD;	PRT;	249 AA.
AC	P17931; Q16005; Q96J47;			
DT	01-NOV-1990 (Rel. 16, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Galectin-3 (Galactose-specific lectin 3) (MAC-2 antigen) (IgE-binding protein) (35 kDa lectin) (Carbohydrate binding protein 35) (CBP 35)			
DE	(Laminin-binding protein) (Lectin L-29) (L-31) (Galactoside-binding protein) (GALBP).			
GN	LGALS3 OR MAC2			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91084480; PubMed=2261464;			
RA	Robertson M.W., Albrandt K., Keller D., Liu F.-T.;			
RT	"Human IgE-binding protein: a soluble lectin exhibiting a highly conserved interspecies sequence and differential recognition of IgE glycoforms.";			
RT	Biochemistry 29:8093-8100(1990).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	TISSUE=Carcinoma;			
RA	MEDLINE=90384999; PubMed=2402511;			
RX	Cherayil B., Chaitovitz S., Wong C., Pillai S.;			
RT	"Molecular cloning of a human macrophage lectin specific for galactose.";			
RT	Proc. Natl. Acad. Sci. U.S.A. 87:7324-7328(1990).			
RL	[3]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=91216471; PubMed=2022338;			
RX	Oda Y., Leffler H., Sakakura Y., Kasai K.I., Barondes S.H.;			
RT	"Human breast carcinoma cDNA encoding a galactoside-binding lectin homologous to mouse Mac-2 antigen.";			
RT	Gene 99:279-283(1991).			
RL	[4]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=91183475; PubMed=2009535;			
RX	Raz A., Carmi P., Raz T., Hogan V., Mohamed A., Wolman S.R.;			
RT	"Molecular cloning and chromosomal mapping of a human galactoside-binding protein.";			
RT	Cancer Res. 51:2173-2178(1991).			
RN	[5]			
RP	SEQUENCE FROM N.A., AND SUBCELLULAR LOCATION.			
RX	MEDLINE=9324518; PubMed=7682704;			
RA	Lotz M.M., Andrews C.W. Jr., Kozellus C.A., Lee E.C.,			
RA	Steele G.D. Jr., Clarke A., Mercurio A.M.;			
RT	"Decreased expression of Mac-2 (carbohydrate binding protein 35) and loss of its nuclear localization are associated with the neoplastic progression of colon carcinoma.";			
RT	Proc. Natl. Acad. Sci. U.S.A. 90:3466-3470(1993).			
RL	[6]			

34	174.5	12.9	299	1	CC34_CAEEL	P34687 caenorhabdi
35	173.5	12.8	266	1	YXWK_CAEEL	Q21184 caenorhabdi
36	173.5	12.8	512	1	ANX7_XENLA	Q92125 xenopus lae
37	173.5	12.8	754	1	CA54_CANFA	Q28247 canis famil
38	173	12.7	135	1	LEG7_MOUSE	O54974 mus musculu
39	173	12.7	675	1	CA39_CHICK	P32017 gallus gall
40	172.5	12.7	1464	1	CA13_MOUSE	Q15428 caenorhabdi
41	172	12.7	301	1	CC02_CAEEL	P17656 caenorhabdi
42	171.5	12.6	464	1	S3A2_HUMAN	Q15428 homo sapien
43	171.5	12.6	1712	1	CA24_HUMAN	P08572 homo sapien
44	170	12.5	1466	1	CA13_HUMAN	P02461 homo sapien
45	169.5	12.5	302	1	CCDC_CAEEL	P17657 caenorhabdi

ALIGNMENTS

RP SEQUENCE FROM N.A.
RC TISSUE-Gastric adenocarcinoma;
RA Kato S.;
RT "Human galectin-3 full-length cDNA";
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RA Kadrofske M.M., Wang J.L.;
RT Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE FROM N.A.
RC TISSUE-Skin;
RA Strausberg R.;
RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [9]
RP PHOSPHORYLATION
RA MEDLINE-94075369; PubMed-8253806;
RT Huffelt M.E., Turck C.W., Lindstedt R., Barondes S.H., Leffler H.;
RT "L-29, a soluble lactose-binding lectin, is phosphorylated on serine
6 and serine 12 in vivo and by casein kinase I.";
RL J. Biol. Chem. 268:26712-26718(1993).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 113-249.
RA MEDLINE-98250755; PubMed-9582341;
RA Seetharaman J., Kanigsberg A., Slaaby R., Leffler H., Barondes S.H.,
RA Rini J.M.;
RT "X-ray crystal structure of the human galectin-3 carbohydrate
recognition domain at 2.1-A resolution.";
RL J. Biol. Chem. 273:13047-13052(1998).
CC -1- FUNCTION: GALACTOSE-SPECIFIC LECTIN WHICH BINDS IGE.
CC -1- SUBUNIT: PROBABLY FORMS HOMO- OR HETERODIMERS.
CC -1- SUBCELLULAR LOCATION: NUCLEAR, CYTOPLASMIC IN ADENOMAS AND
CC CARCINOMAS.
CC -1- TISSUE SPECIFICITY: A MAJOR EXPRESSION IS FOUND IN THE COLONIC
CC EPITHELIUM. IT IS ALSO ABUNDANT IN THE ACTIVATED MACROPHAGES.
CC -1- SIMILARITY: THE C-TERMINAL DOMAIN BELONGS TO THE GALAPTIN
CC (S-LECTIN) FAMILY.
CC -----
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CC -----
DR EMBL; M57710; AAA35607.1; -;
DR EMBL; M35368; AAA8086.1; -;
DR EMBL; M36582; AAA36163.1; -;
DR EMBL; M64303; -; NOT_ANNOTATED_CDS.
DR EMBL; S59012; AAB26229.1; -;
DR EMBL; AB006780; BAA22164.1; -;
DR EMBL; AF031425; AAB86584.1; -;
DR EMBL; AF031423; AAB86584.1; JOINED.
DR EMBL; AF031422; AAB86584.1; JOINED.
DR EMBL; AF031424; AAB86584.1; JOINED.
DR EMBL; BC001120; AAB01120.1; -;
DR PIR; A35820; A35820.
DR PIR; A36071; A36071.
DR PIR; JQ0916; JQ0916.
DR PDB; 1A3K; 15-JUL-98.
DR Genew; HGNC:6563; LGALS3.
DR MIM; 153619; -;
DR InterPro; IPR001079; Galectin.
DR Pfam; PF00337; Gal-bind_lectin; 1.
DR SMART; SM00276; GLECT; 1.
DR PROSITE; PS00309; GALAPTIN; 1.
KW Galaptin; Lectin; IGE-binding protein; Repeat; Phosphorylation;
KW Acetylation; Nuclear protein; Polymorphism; 3D-structure.
FT INIT_MET 0 0 BY SIMILARITY.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT MOD_RES 5 5 PHOSPHORYLATION.
FT MOD_RES 11 11 PHOSPHORYLATION (MINOR).

FT DOMAIN 35 108 8 X 9 AA TANDEM REPEATS OF Y-P-G-X(3)-P-
FT REPEAT 35 43 G-A.
FT REPEAT 44 52 1.
FT REPEAT 53 61 2.
FT REPEAT 62 68 3.
FT REPEAT 69 77 4 (APPROXIMATE).
FT REPEAT 78 87 5.
FT REPEAT 88 99 6 (APPROXIMATE).
FT REPEAT 100 108 7 (APPROXIMATE).
FT REPEAT 117 129 8 (APPROXIMATE).
FT DISULFID 172 249 GALAPTIN.
FT BINDING 180 186 INTERCHAIN (BY SIMILARITY).
FT VARIANT 63 63 BETA-GALACTOSIDE (BY SIMILARITY).
FT VARIANT 97 97 H -> P.
FT VARIANT 97 97 /FTID=VAR_012988.
FT VARIANT 97 97 P -> T.
FT CONFLICT 32 51 /FTID=VAR_012989.
FT CONFLICT 87 87 AGGPGASIPGAYPGQAPPG -> QGLPRGFLSWGLPRAGT
FT CONFLICT 231 231 PR (IN REF. 2).
FT CONFLICT 249 AA; 26057 MW; ACB542752D137650 CRC64;
SQ SEQUENCE 249 AA; 26057 MW; ACB542752D137650 CRC64;
Query Match 96.5%; Score 1310; DB 1; Length 249;
Best Local Similarity 98.4%; Pred. NO. 2.4e-74;
Matches 245; Conservative 0; Mismatches 0; Indels 4; Gaps 4;
QY 2 ADNFSLDALSGSGNPNPQGWPGAWGNQAGAGYPCGASYPG-YPGQAPPGAYPGQAPPG 60
DB 1 ADNFSLDALSGSGNPNPQGWPGAWGNQAGAGYPCGASYPGAYPGQAPPGAYPGQAPPG 60
QY 61 AYHGAPGAYGAPAGPYPGPPSGGAYPSGGQSPAGAY-ATGPGAPAGPLIVPNLP 119
DB 61 AYHGAPGAYGAPAGPYPGPPSGGAYPSGGQSPAGAYPATGPGYCAPAGPLIVPNLP 120
QY 120 LPGGVPRMLITILGTVPKPNANRIALDFQGNDAVFHF-PRENENRRVIVCNTKLDNNW 178
DB 121 LPGGVPRMLITILGTVPKPNANRIALDFQGNDAVFHF-PRENENRRVIVCNTKLDNNW 180
QY 179 GREERQSVFFESGKPKIQVLVEPDHFKVAVNDAH-LOYNHRVKKLEISKLGISGDID 237
DB 181 GREERQSVFFESGKPKIQVLVEPDHFKVAVNDAHLOYNHRVKKLEISKLGISGDID 240
QY 238 LTSASYTMI 246
DB 241 LTSASYTMI 249
RESULT 2
LEG3_CANFA STANDARD; PRT; 295 AA.
ID LEG3_CANFA
AC P38486;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Galectin-3 (Galactose-specific lectin 3) (MAC-2 antigen) (IGE-binding
DE protein) (35 kDa lectin) (Carbohydrate binding protein 35) (CBP 35)
DE (Laminin-binding protein) (Lectin L-29).
GN LGALS3.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE OF 11-295 FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE-Kidney epithelium;
RX MEDLINE-94075368; PubMed-8253805;
RA Herrmann J., Turck C.W., Atchison R.E., Huffelt M.E., Poulter L.,
RA Gitt M.A., Burlingame A.L., Barondes S.H., Leffler H.;
RT "Primary structure of the soluble lactose binding lectin L-29 from
RT rat and dog and interaction of its non-collagenous proline-,
RT glycine-, tyrosine-rich sequence with bacterial and tissue
RT collagenase.";
RN [1]

RL J. Biol. Chem. 268:26704-26711(1993).
 RN [2]
 RP PHOSPHORYLATION.
 RX MEDLINE=94075369; PubMed=8253806;
 RA Hufelt M.E., Turk C.W., Lindstedt R., Barondes S.H., Leffler H.;
 RT "L-29, a soluble lactose-binding lectin, is phosphorylated on serine
 6 and serine 12 in vivo and by casein kinase I.";
 RL J. Biol. Chem. 268:26712-26718(1993).
 CC -1- FUNCTION: GALACTOSE-SPECIFIC LECTIN WHICH BINDS IGE.
 CC -1- SUBUNIT: PROBABLY FORMS HOMO- OR HETERODIMERS.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC. MAY BE SECRETED BY
 CC A NON-CLASSICAL SECRETORY PATHWAY.
 CC -1- PTM: THE DEGREE OF PHOSPHORYLATION IS HIGHER IN THE CYTOPLASMIC
 CC FORM THAN IN THE NUCLEAR FORM.
 CC -1- SIMILARITY: THE C-TERMINAL DOMAIN BELONGS TO THE GALAPTIN
 CC (S-LECTIN) FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L23429; AAA16211.1; -;
 DR HSSP; P17931; 1A3K.
 DR InterPro; IPR001079; Galectin.
 DR Pfam; PF00337; Gal-bind_lectin; 1.
 DR SMART; SM00276; GLECT; 1.
 DR PROSITE; PS00309; GALAPTIN; 1.
 DR Galaptin; Lectin; IGE-binding protein; Repeat; Phosphorylation;
 KW Acetylation; Nuclear protein.
 FT INIT_MET 0
 FT MOD_RES 1 1
 FT MOD_RES 5 5
 FT MOD_RES 11 11
 FT MOD_RES 35 142
 FT DOMAIN 35 142
 FT REPEAT 35 43
 FT REPEAT 44 52
 FT REPEAT 53 61
 FT REPEAT 62 70
 FT REPEAT 71 79
 FT REPEAT 80 88
 FT REPEAT 89 97
 FT REPEAT 98 106
 FT REPEAT 107 114
 FT REPEAT 115 123
 FT REPEAT 124 133
 FT REPEAT 134 142
 FT REPEAT 152 295
 FT DOMAIN 152 295
 FT DISULFID 218 218
 FT BINDING 226 232
 FT SEQUENCE 295 AA; 30199 MW; 4921327063CE41C7 CRC64;
 Query Match 80.4%; Score 1091; DB 1; Length 295;
 Best Local Similarity 71.2%; Pred. No. 8.2e-61;
 Matches 210; Conservative 13; Mismatches 22; Indels 50; Gaps 6;
 QY 2 ADNFSLDALSGGNPNQGWPCAGNGNPAGAGGYPGASYP----- 42
 DB 1 ADSFSLDALSGGNPNQGWPCAGNGNPAGAGGYPGASYPGAYPGQAPPGYQAPPG 60
 QY 43 -----GYPGQAPPGYQAPPGYAHG--APGAYPGAPGYPGP----- 81
 DB 61 GYPGQAPPGYQAPPGYQAPPGYQAPPGYQAPPGYQAPPGYQAPPGYQAPPGYPTA 120
 QY 82 -----PSGRCAYSSGQPSARGAY-ATGPYAGAPGLIVPNLPLPGGVPRMLITIL 133
 DB 121 PGTQPGSGGAYPPPGQPSAPGAYPAAGPGIPAGLTVPDYDLPPLPGGVKPRMLITIL 180

QY 134 GTVKPNANRIALDFQNDVAFHF-PRENNRRVIVCNTKLDNNWGREROSVFFPESG 192
 DB 181 GTVRSANRLALDFKRGNDVAFHFPRFEDNKRIVICNTKLDNIWCKEERQAFFESG 240
 QY 193 KPEKQVLVEPDHFHGVANDAH-LQYNHRVKKLNEISKLGISGIDILTSASYTMI 246
 DB 241 KPEKIQVLVESDHFHGVANDAHLLQYNHRMKNLPEISKLGISGIDILTSASYAMI 295
 RESULT 3
 LEG3_MOUSE
 ID LEG3_MOUSE STANDARD; PRT; 263 AA.
 AC P16110;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Galectin-3 (Galactose-specific lectin 3) (MAC-2 antigen) (IGE-binding
 DE protein) (35 kDa lectin) (Carbohydrate binding protein 35) (CBP 35)
 DE (Laminin-binding protein) (Lectin L-29) (L-34 galactoside-binding
 DE lectin).
 GN LGALS3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DBA/2J; TISSUE=Macrophage;
 RX MEDLINE=90063462; PubMed=2584931;
 RA Cherayil B.J., Weiner S.J., Pillai S.;
 RT "The Mac-2 antigen is a galactose-specific lectin that binds IGE.";
 RL J. Exp. Med. 170:1959-1972(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88198129; PubMed=3360772;
 RA Jia S., Wang J.L.;
 RT "Carbohydrate binding protein 35. Complementary DNA sequence reveals
 RT homology with proteins of the heterogeneous nuclear RNP.";
 RL J. Biol. Chem. 263:6009-6011(1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89275058; PubMed=2525069;
 RA Raz A., Pazerini G., Carmi P.;
 RT "Identification of the metastasis-associated, galactoside-binding
 RT lectin as a chimeric gene product with homology to an IGE-binding
 RT protein.";
 RL Cancer Res. 49:3489-3493(1989).
 RN [4]
 RP SEQUENCE OF 158-162; 165-174 AND 213-225.
 RX MEDLINE=90236991; PubMed=2332426;
 RA Woo H.-J., Shaw L.M., Messier J.M., Mercurio A.M.;
 RT "The major non-integrin laminin binding protein of macrophages is
 RT identical to carbohydrate binding protein 35 (Mac-2).";
 RL J. Biol. Chem. 265:7097-7099(1990).
 RN [5]
 RP DISULFIDE BOND.
 RX MEDLINE=92011585; PubMed=1917966;
 RA Woo H.-J., Lotz M.M., Jung J.U., Mercurio A.M.;
 RT "Carbohydrate-binding protein 35 (Mac-2), a laminin-binding lectin,
 RT forms functional dimers using cysteine 186.";
 RL J. Biol. Chem. 266:18419-18422(1991).
 CC -1- FUNCTION: GALACTOSE-SPECIFIC LECTIN WHICH BINDS IGE.
 CC -1- SUBUNIT: EXISTS AS SEVERAL DISTINCT SPECIES OF 35, 67 AND 80 KDa.
 CC PROBABLY FORMS HOMO- OR HETERODIMERS.
 CC -1- TISSUE SPECIFICITY: THE HIGHEST LEVELS ARE FOUND IN ACTIVATED
 CC MACROPHAGES.
 CC -1- SIMILARITY: THE C-TERMINAL DOMAIN BELONGS TO THE GALAPTIN
 CC (S-LECTIN) FAMILY.
 CC -----
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CC EMBL; X16834; CAA34736.1; -
CC EMBL; J03723; AAA37311.1; -
CC EMBL; X16074; CAA34206.1; -
CC PIR; A28651; A28651.
CC PIR; A35185; A35185.
CC PIR; S08537; S08537.
CC HSP; P17931; IA3K.
CC MGD; MGI:96778; Lgals3.
CC InterPro; IPR001079; Galectin.
CC Pfam; PF00337; Gal_bind_lectin; 1.
CC SMART; SM00276; GLECT; 1.
CC PROSITE; PS00309; GALAPTIN; 1.
CC Galaptin; Lectin; IgE-binding protein; Repeat; Phosphorylation;
KW Acetylation.
FT INIT_MET 0 0 BY SIMILARITY.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT MOD_RES 5 5 PHOSPHORYLATION (BY CK1).
FT 9 X 9 AA TANDEM REPEATS OF Y-P-G-X(3)-P-
FT DOMAIN 34 113 [GS]-A.
FT REPEAT 34 42 1.
FT REPEAT 43 51 2.
FT REPEAT 52 60 3.
FT REPEAT 61 69 4.
FT REPEAT 70 78 5.
FT REPEAT 79 87 6.
FT REPEAT 88 96 7.
FT REPEAT 97 106 8.
FT REPEAT 107 113 9 (INCOMPLETE).
FT DOMAIN 131 263 GALAPTIN.
FT DISULFID 186 186 INTERCHAIN.
FT BINDING 194 200 BETA-GALACTOSIDE (BY SIMILARITY).
FT CONFLICT 1 1 A -> R (IN REF. 2).
FT CONFLICT 3 3 S -> T (IN REF. 3).
FT CONFLICT 91 92 QP -> ST (IN REF. 3).
FT CONFLICT 109 111 QCS -> SAP (IN REF. 3).
FT CONFLICT 251 251 G -> R (IN REF. 2).
FT SEQUENCE 263 AA; 27384 MW; 76C78AA0810D68EE CRC64;
Query Match 79.4%; Score 1077; DB 1; Length 263;
Best Local Similarity 77.9%; Pred. No. 5.3e-60;
Matches 208; Conservative 16; Mismatches 17; Indels 26; Gaps 8;
Qy 2 ADNFSLDALSGSNPNQGWPGWGNOPACAGGYGPGASYPG-YPGQAPPGAYPGQAPPG 60
Db 1 ADSFSLDALAGSNPNQGWPGWGNOP-GAGGYPGAYPGAYPGQAPPGAYPGQAPPG 59
Qy 61 AYHG-----APGAYPGAPGAYPGYPPSPGAYPSGQPSAPGAY-----A 101
Db 60 AYPGQAPPSAYPGPTAPGAYPGTAPGAYPGQPA-PGAFP--GPGAPGAYPGQSGGYP 116
Qy 102 TGPYGAPAGPLIVPNLPLPGGVPRMLITILGTVPKPNANRIALDFQGNDAVFHF-PRF 160
Db 117 AGPYGVPAGPLTPYDPLPGGVPRMLITIMGTVPKPNANRIALDFRGNDAVFHFNPRF 176
Qy 161 NENNRVIVCNKTLKNNNGREOSVFPESGKPKIQVLVEPDHFKVAVNDAAH-LQYNH 219
Db 177 NENNRVIVCNKTDNNNGREOSVFPESGKPKIQVLVEADHFKVAVNDAAHLLQYNH 236
Qy 220 RVKLNLEISKLGISGIDLTLSASTMI 246
Db 237 RMKNLREISQLGISGIDLTLSANHAMI 263
PRT; 261 AA.
STANDARD;
LEG3_RAT
AC P08699;

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DT 01-JAN-1988 (Rel. 06, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Galectin-3 (Galactose-specific lectin 3) (MAC-2 antigen) (IgE-binding
DE protein) (35 kDa lectin) (Carbohydrate binding protein 35) (CBP 35)
DE (Laminin-binding protein) (Lectin L-29).
DE LGALS3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=88016189; PubMed=2958848;
RA Albrandt K., Orida N.K., Liu F.-T.;
RT "An IgE-binding protein with a distinctive repetitive sequence and
RT homology with an IgG receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:6859-6863(1987).
[2]
SEQUENCE OF 124-261 FROM N.A.
RP MEDLINE=85216641; PubMed=3858867;
RA Liu F.-T., Albrandt K., Mendel E., Kulczycki A. Jr., Orida N.K.;
RT "Identification of an IgE-binding protein by molecular cloning.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:4100-4104(1985).
[3]
SEQUENCE OF 119-144.
RP MEDLINE=90105471; PubMed=2605254;
RA Lefler H., Maslarz F.R., Barondes S.H.;
RT "Soluble lactose-binding vertebrate lectins: a growing family.";
RL Biochemistry 28:9222-9229(1989).
[4]
PARTIAL SEQUENCE, AND ACETYLATION.
RP MEDLINE=94075368; PubMed=8253805;
RA Herrmann J., Turck C.W., Atchison R.E., Hufelt M.E., Poulter L.,
RA Gitt M.A., Burlingame A.L., Barondes S.H., Leffler H.;
RT "Primary structure of the soluble lactose binding lectin L-29 from
RT rat and dog and interaction of its non-collagenous proline-,
RT glycine-, tyrosine-rich sequence with bacterial and tissue
RT collagenase.";
RL J. Biol. Chem. 268:26704-26711(1993).
CC -|- FUNCTION: GALACTOSE-SPECIFIC LECTIN WHICH BINDS IGE.
CC -|- SUBUNIT: PROBABLY FORMS HOMO- OR HETERODIMERS.
CC -|- SIMILARITY: THE C-TERMINAL DOMAIN BELONGS TO THE GALAPTIN
CC (S-LECTIN) FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).

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RESULT 4
LEG3_RAT
ID LEG3
AC P08699;

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FT REPEAT 61 69 4.
FT REPEAT 70 78 5.
FT REPEAT 79 87 6.
FT REPEAT 88 97 7 (APPROXIMATE).
FT REPEAT 98 104 8 (APPROXIMATE).
FT REPEAT 105 111 9 (INCOMPLETE).
FT DOMAIN 129 261 GALAPTIN.
FT DISULFID 184 184 INTERCHAIN (BY SIMILARITY).
FT BINDING 192 198 BETA-GALACTOSIDE (BY SIMILARITY).
FT CONFLICT 19 19 O -> R (IN REF. 1).
SQ SEQUENCE 261 AA; 27070 MW; EAFAL17F5EA5080D CRC64;

Query Match
Best Local Similarity 79.1%; Score 1074; DB 1; Length 261;
Matches 204; Conservative 16; Mismatches 24; Indels 18; Gaps 7;

QY 2 ADNFSLDALSGSGNPNQPGWPGANGNPGAGGYPGASYPG-YPCOAPPGAYPGQAPPG 60
DB 1 ADGFSLDALSGSGNPNQPGWPGANGNPGAGGYPGASYPGAYPGQAPPGYPGQAPPS 59
QY 61 AYHG-----APGAYPCAPAPGVYPPGPGSGAYPSS--GQSPAGAY-ATGPGY 106
DB 60 AYPGTPGSAYPGAPGAPGTPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGP 119
QY 107 APAGPLIYVYNPLPGGVVPRMLITIGTVKPNANRIALDFORGNDAVHF-PRFNENNR 165
DB 120 APTGLTVPYDPLPGGVNPRMLITIGTVKPNANSITLNFKKGNDAIAPHFNPRFNENNR 179
QY 166 RIVCNTKLDNNGREOSVFPESGKPKIQVLVEPDHFKVAVNDAH-LOYNHRVKKL 224
DB 180 RIVCNTKODNNGREOSVFPESGKPKIQVLVEPDHFKVAVNDAHLLQYNHRMKNL 239
QY 225 NEISKLGISGDIDLSASYTMI 246
DB 240 REISQLGIIGDITLSASHAMI 261

RESULT 5
LEG3_CRILO STANDARD; PRT; 244 AA.
AC P47953;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Galectin-3 (Galactose-specific lectin 3) (MAC-2 antigen) (IgE-binding protein) (35 kDa lectin) (Carbohydrate binding protein 35) (CBP 35)
DE (Laminin-binding protein) (Lectin L-29) (CBP30).
GN LGALS3.
OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Cricetulus.
OX NCBI_TaxID=10030;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA MEDLINE=94299546; PubMed=8027086;
RX Mehul B., Bawumia S., Martin S.R., Hughes R.C.;
RT "Structure of baby hamster kidney carbohydrate-binding protein CBP30, an S-type animal lectin."
RL J. Biol. Chem. 269:18250-18258(1994).
CC -!- FUNCTION: GALACTOSE-SPECIFIC LECTIN WHICH BINDS IGE.
CC -!- SIMILARITY: THE C-TERMINAL DOMAIN BELONGS TO THE GALAPTIN (S-LECTIN) FAMILY.
CC -----
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CC -----

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DR EMBL; X78879; CAA55479.1; -.
DR HSSP; PI7931; IA3K.
DR InterPro; IPR001079; Galectin.
DR Pfam; PF00337; Gal-bind_lectin; 1.
DR SMART; SM00276; GLECT; 1.
DR PROSITE; PS00309; GALAPTIN; 1.
KW Galaptin; Lectin; IgE-binding protein; Repeat; Phosphorylation;
KW Acetylation.
FT INIT_MET 0 0 BY SIMILARITY.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT MOD_RES 5 5 PHOSPHORYLATION (BY CK1)
FT DOMAIN 34 98 (BY SIMILARITY).
FT REPEAT 34 42 1.
FT REPEAT 43 51 2.
FT REPEAT 52 60 3.
FT REPEAT 61 69 4.
FT REPEAT 70 77 5 (APPROXIMATE).
FT REPEAT 78 87 6 (APPROXIMATE).
FT REPEAT 88 98 7 (APPROXIMATE).
FT DOMAIN 112 244 GALAPTIN.
FT DISULFID 167 167 INTERCHAIN (BY SIMILARITY).
FT BINDING 175 181 BETA-GALACTOSIDE (BY SIMILARITY).
SQ SEQUENCE 244 AA; 25608 MW; 8F99B9AA0BBA7D3F CRC64;

Query Match
Best Local Similarity 77.0%; Score 1044.5; DB 1; Length 244;
Matches 203; Conservative 12; Mismatches 23; Indels 13; Gaps 8;

QY 2 ADNFSLDALSGSGNPNQPGWPGANGNPGAGGYPGASYPG-YPGQAPPGAYPGQAPPG 60
DB 1 ADGFSLDALSGSGNPNQPGWPGANGNPGAGGYPGASYPGAYPGQAPPGYPGQAPPS 59
QY 61 AYHG--APGAYPCAPAPGVYPPGPGSGAYPSSGQSPAGAY-ATGPGYCAPAGPLIYVYN 117
DB 60 AYPGTPAGAYPG-PAPGAYPGQPGASGAY-----PSAFGAYPAGPYGAPTGAITVYK 113
QY 118 LPLPGGVPRMLITIGTVKPNANRIALDFORGNDAVHF-PRFNENNRVIVCNTKLDN 176
DB 114 LPLAGVMPRLITIGTVKPNANRIALDFORGNDAVHF-PRFNENNRVIVCNTKLDN 173
QY 177 NMGREERQSVFPESGKPKIQVLVEPDHFKVAVNDAH-LOYNHRVKKLEISKLGISGD 235
DB 174 NMGREERQSAFPESGKPKIQVLVEADHFKVAVNDAHLLQYNHRMKNLEINQMEISGD 233
QY 236 IDLTSASYTMI 246
DB 234 ITLTSAAPTMI 244

RESULT 6
LEG3_RABIT STANDARD; PRT; 241 AA.
AC P47845;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Galectin-3 (Galactose-specific lectin 3) (MAC-2 antigen) (IgE-binding protein) (35 kDa lectin) (Carbohydrate binding protein 35) (CBP 35)
DE (Laminin-binding protein) (Lectin L-29).
GN LGALS3.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=New Zealand white; TISSUE=Aorta;
RX MEDLINE=96011642; PubMed=7590275;
RA Gaudin J.-C., Monsigny M., Legrand A.;
RT "Cloning of the cDNA encoding rabbit galectin-3."
RL Gene 163:249-252(1995).

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Query Match          17.4%; Score 236.5; DB 1; Length 324;
Best Local Similarity 35.2%; Pred. No. 3e-08;
Matches 68; Conservative 25; Mismatches 63; Indels 37; Gaps 10;

71 GAPAGVYVPGPPSGGAYPSSGOPSAPGAYATGYGAP-----AGPLI-----VPYNL 118
   ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| |||
152 GQPAASQYVPGTWTIP-AYPSAG-----YNPQMNSLPYMGPPPIENPPVPYVG 198
   ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| |||

119 PLPGGVVPRMLITILGVTKVKNANRIALDFORGN--DVAFHF-PRFNNRRRVIVCNKLD 175
   ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| |||
199 TLOGGLTARTIIITKGYVLPTAKNLIINFKVGSTGDI AFHMPNPRIGD-----CVRNSYMN 254
   ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| |||

176 NNWGRETSQSVF-PFESGPKFKIOVLPEPHFKVAVYNDAAHL-QYNHRVKKLNEISKLGIS 233
   :|| ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
255 GSWSEEEKIPYNPFPGAQGFDSIRCTDRFKVFANGQHLDFSHRFQAFQFQVDMLEIK 314
   :|| ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||

234 GDIDLTASVYMI 246
   ||| ||| |||
315 GDITL---SYVQI 324
   ||| ||| |||

RESULT 14.
LEG8_HUMAN
IID LEG8_HUMAN STANDARD; PRT; 316 AA.
AAC 000214; Q15215; Q9UP34; Q9UEZ6; Q9UP33; Q9UP32; Q9H584; Q9H585;
Q96B92;
01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galectin-8 (Gal-8) (Prostate carcinoma tumor antigen 1) (PCTA-1)
(Po66 carbohydrate-binding protein) (Po66-CBP).
LGALS8.
Homo sapiens (Human).
OOS Homo sapiens (Human).
OOC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OOC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RN RP TISSUE=Prostate;
RN RP MEDLINE=96293510; PubMed=8692978;
RN RP Su Z.-Z., Lin J., Shen R., Fisher P.E., Goldstein N.I., Fisher P.B.;
RA "Surface-epitope masking and expression cloning identifies the human
RRT prostate carcinoma tumor antigen gene PCTA-1 a member of the galectin
RRT gene family.";
RRT Proc. Natl. Acad. Sci. U.S.A. 93:7252-7257(1996).
[2]
RN RP SEQUENCE FROM N.A.
RN RP TISSUE=Hippocampus;
RN RP Hadari Y.R., Eisenstein M., Zakut R., Zick Y.;
RA "Galectin-8: on the road from structure to function.";
RRT Trends Glycosci. Glycotechnol. 9:103-112(1997).
[3]
RN RP SEQUENCE FROM N.A.; AND ALTERNATIVE SPLICING.
RN RP TISSUE=Lung carcinoma;
RA Brichory F., Bidon N., Desrues B., Bourguet P., Le Pennec J.P.,
RA Dazord L.;
RA "Molecular cloning of a beta-galactoside-binding lectin related to
RRT galectin-8 and identified in human lung carcinoma.";
RRT Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
[4]
RN RP SEQUENCE FROM N.A.
RN RP Walter C., Haeussler J., Roesch K., Moschgath E., Vogel W.;
RA "Genomic organization and expression of the human galectin-8 gene.";
RRT Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
[5]
RN RP SEQUENCE FROM N.A.
RN RP MEDLINE=20438187; PubMed=10980616;
RX Gopalakrishnan R.V., Roberts T., Tuli S., Kang D., Christiansen K.A.,
RA Fisher P.B.;
RA "Molecular characterization of prostate carcinoma tumor antigen-1,
RRT PCTA-1, a human galectin-8 related gene.";
RRL Oncogene 19:4405-4416(2000).
[6]
RN RP

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SQ SEQUENCE 316 AA; 35538 MW; 1724C36085A0510A CRC64;
Query Match 16.8%; Score 228.5; DB 1; Length 316;
Best Local Similarity 40.0%; Pred. No. 9e-08;
Matches 56; Conservative 22; Mismatches 51; Indels 11; Gaps 5;

QY 113 IVPYNLPLGGVVRMLITILGTVKPNANRIALDFQRN-----DVAFHF-PRENNR 165
      :|| :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 15 VIPVGTPDLPDGLTLCVGHVPSADRFQVDLQNGSSVKPRADVAFHFNPKRAG- 73
      :|| :| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 166 RVIVCNTKLDNNWGRERQSFPPECKPKIQVLVEPHFKVAVNDAAH-LQYNHRVKKL 224
      ||||| :| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 74 -CIVCNLTLINEKGWRREITYDTFKREKSFSEIWMUKDRFQAVANGKHTLLYGHRIGP- 131
      :|| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 225 NETSKLGISGDIDLTASYT 244
      :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 132 EKIDTLGIYKVNIHSIGFS 151
      :| | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 15
LEG8_RAT STANDARD; PRT; 316 AA.
AC Q62665;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last annotation update)
DE Galectin-8 (30 kDa S-type lectin) (RL-30).
GN LGALS8
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=95155445; PubMed=7852431;
RA Hadari Y.R., Paz K., Dekel R., Mestrovic T., Accilli D., Zick Y.;
RT "Galectin-8. A new rat lectin, related to galectin-4.";
RL J Biol. Chem. 270:3447-3453(1995).
CC -1- FUNCTION: POSSIBLE SUGAR BINDING AND HEMAGGLUTINATION ACTIVITY.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, KIDNEY, CARDIAC MUSCLE,
CC LUNG, AND BRAIN.
CC -1- DEVELOPMENTAL STAGE: VERY LOW LEVELS IN WHOLE EMBRYOS, HIGH LEVELS
CC IN ADULT TISSUES.
CC -1- DOMAIN: CONTAINS TWO HOMOLOGOUS BUT DISTINCT CARBOHYDRATE-BINDING
CC DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE GALAPTIN (S-LECTIN) FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U09824; AAA66359.1; --
DR HSP; P17931; IA3K.
DR InterPro; IPR001079; Galectin.
DR Pfam; PF00337; Gal-bind_lectin; 2.
DR SMART; SM00276; GLECT; 2.
DR PROSITE; PS00309; GALAPTIN; 1.
KW Galaptin; Lectin; Repeat.
FT DOMAIN 1 153 GALAPTIN 1.
FT FT DOMAIN 154 184 LINKER.
FT FT DOMAIN 185 316 GALAPTIN 2.
FT FT BINDING 248 254 BETA-GALACTOSIDE (BY SIMILARITY).
SQ SEQUENCE 316 AA; 36038 MW; C04B766CFE913D59 CRC64;

Query Match 16.1%; Score 218.5; DB 1; Length 316;
Best Local Similarity 39.9%; Pred. No. 3.7e-07;
Matches 55; Conservative 18; Mismatches 54; Indels 11; Gaps 5;

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QY 114 VPYNPLPGGVVPRMLTILGTVPKNANRIALDEQRGN-----DVAHF-PRFNNRR 166
:| | : | | | | | : | | | | | :| | :|
Db 16 IPYVSTITEQLKPGSLIVIRGHVPKDSERFQVDFHGNLSLKPRADVAHFENPRFKRSN-- 73
:| | : | | | | | : | | | | | :| | :|
QY 167 VIVCNTKLDNNWGREERQSVFPESGPKFQVLEPDHFKVAVNDAH-LQYNHRVKLN 225
:| | : | | | | | : | | | | | :| | :|
Db 74 CIVCNTLTNEKGWEEITHDMPFRKESFEIVIMVLANKFHVAVNGKHILLYAHRNP-E 132
:| | : | | | | | : | | | | | :| | :|
QY 226 EISKLGISGDIDLTASY 243
:| | : | | | | | : | | | | | :| | :|
Db 133 KIDTLGIEGKVNHSIGF 150
:| | : | | | | | : | | | | | :| | :|

Search completed: May 20, 2003, 12:18:53
Job time : 12 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 20, 2003, 12:16:45 ; Search time 34 Seconds
(without alignments)
1490.811 Million cell updates/sec

Title: US-09-297-040-4
Perfect score: 1357
Sequence: 1 MADNFSLHDALSGGNPNPQ.....ISKLGISGIDILFSASYTMI 246

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_verticillate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	768	56.6	186	11 Q9CVE3	Q9cve3 mus musculus
2	695.5	51.3	262	13 Q90713	Q90713 gallus gall
3	663.5	48.9	332	13 Q8QGD9	Q8qgd9 gallus gall
4	444	32.7	139	11 Q61357	Q61357 mus musculus
5	314.5	23.2	341	13 Q9PRL1	Q9ptl1 oncorhynch
6	299	22.0	322	11 Q99183	Q99183 mus musculus
7	271	20.0	348	13 Q8QCB1	Q8qcb1 oncorhynch
8	264	19.5	311	4 Q8WY07	Q8wyg7 homo sapien
9	260	19.2	349	6 Q9XSM9	Q9xsm9 sus scrofa
10	258	19.0	343	13 Q8UW98	Q8uw98 xenopus lae
11	257	18.9	317	6 Q9XSM8	Q9xsm8 sus scrofa
12	246.5	18.2	340	13 Q8UW99	Q8uw99 xenopus lae
13	243.5	17.9	326	11 Q91X74	Q91x74 mus musculus
14	233.5	17.2	328	6 Q9TUB8	Q9tub8 oryctolagus
15	228.5	16.8	359	4 Q8TEV1	Q8tev1 homo sapien
16	223.5	16.5	359	4 Q9BXC8	Q9bxc8 homo sapien

17	216.5	16.0	300	11 Q88353	Q88353 mus musculus
18	213	15.7	332	13 Q8UW97	Q8uw97 xenopus lae
19	210.5	15.5	703	12 Q83467	Q83467 porcine ade
20	206.5	15.2	162	6 Q8WN59	Q8wn59 ovis aries
21	198	14.6	245	4 Q96BC5	Q96bg5 homo sapien
22	192.5	14.2	463	11 Q922A2	Q922a2 mus musculus
23	190.5	14.0	177	10 Q39115	Q39115 arabidopsis
24	189.5	14.0	329	5 Q44796	Q44796 caenorhabdi
25	188.5	13.9	285	5 Q45904	Q45904 caenorhabdi
26	187.5	13.8	277	5 Q9NJV1	Q9njv1 haemonchus
27	187.5	13.8	283	5 Q9NJV0	Q9njv0 haemonchus
28	187.5	13.8	313	5 Q20922	Q20922 caenorhabdi
29	187	13.8	300	4 Q96Q57	Q96qs7 homo sapien
30	186.5	13.7	179	10 Q9M0L8	Q9m0l8 arabidopsis
31	186.5	13.7	277	10 Q49678	Q49678 arabidopsis
32	185.5	13.7	463	11 Q8VIN2	Q8vin2 rattus norv
33	185	13.6	744	4 Q96D07	Q96d07 homo sapien
34	185	13.6	1070	2 Q9APM8	Q9apm8 myxococcus
35	184	13.6	299	5 Q18302	Q18302 caenorhabdi
36	183.5	13.5	744	11 Q9D2V4	Q9d2v4 mus musculus
37	183.5	13.5	744	11 Q921S8	Q921s8 mus musculus
38	183	13.5	299	5 Q27318	Q27318 caenorhabdi
39	183	13.5	1884	5 Q9NHW2	Q9nhw2 nephila mad
40	182.5	13.4	317	5 Q20091	Q20091 caenorhabdi
41	181.5	13.4	304	5 Q9XVG3	Q9xvg3 caenorhabdi
42	181.5	13.4	304	5 Q9U349	Q9u349 caenorhabdi
43	181.5	13.4	304	5 Q9U348	Q9u348 caenorhabdi
44	181.5	13.4	308	5 Q94620	Q94620 meloidogyne
45	181.5	13.4	462	5 Q9NHW3	Q9nhw3 nephila cla

ALIGNMENTS

RESULT 1

Q9CVE3	ID	Q9CVE3	PRELIMINARY;	PRT;	186 AA.
AC	Q9CVE3;				
DT	01-JUN-2001	(TREMBLrel. 17, Created)			
DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)			
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)			
DE	Lectin, galactose binding, soluble 3 (Fragment).				
GN	LGALS3.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_taxid=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=SMALL INTESTINE;				
RX	MEDLINE=21085660; PubMed=11217851;				
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,				
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,				
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,				
RA	Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,				
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,				
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,				
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,				
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,				
RA	Sakai K., Okido T., Furuno M., Aono H., Baidarelli R., Barsh G.,				
RA	Blake J., Boirelli D., Bojunga N., Carninci P., de Bonaldo M.F.,				
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,				
RA	Gustincich S., Hill D., Hcfmann M., Hume D.A., Kamiya M., Lee N.H.,				
RA	Lyons P., Marchionni L., Washima J., Mazzarelli J., Womberts P.,				
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,				
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,				
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,				
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,				
RT	Hayashizaki Y.				
RT	"Functional annotation of a full-length mouse cDNA collection.";				
RL	Nature 409:685-690(2001).				
DR	EMBL; AK008593; BAB25766.1; -				
DR	HSSP; P17931; 1A3K.				

DR MGD; MGI:96778; Lgals3.
DR InterPro: IPR001079; Galectin.
DR Pfam: PF00337; Gal_bind_lectin; 1.
DR SMART: SM00276; GLECT; 1.
DR PROSITE: PS00309; GALAPTIN; 1.
DR NON_TER 1
SQ SEQUENCE 186 AA; 19938 MW; 0971F91053126996 CRC64;

Query Match 56.6%; Score 768; DB 11; Length 186;
Best Local Similarity 80.0%; Pred. NO. 1.9e-59;
Matches 148; Conservative 11; Mismatches 18; Indels 8; Gaps 4;

Qy 65 APGAYCAPAGPYGPPSGGAYPSGQPSAPGAY-ATGPGAPAGPLIVPNLPLPG 123
Db 7 AGGAYPGSTAPGAPGPGGAPGAY-----PSAPGGTAPGYPVAGPLTVPYDPLPG 61
Qy 124 VVPRMLITILGTVKPNANRIALDFQRNDVAFHF-PRFNENRRVIVCNTKLDNNNGREE 182
Db 62 VMPRLITINGTVKPNANRIALDFQRNDVAFHFPRFNENRRVIVCNTKQDNNNGKEE 121
Qy 183 QSVFPFESGKPFKIQVLVDPDHFKVAVNDAH-LOYNHRVKKLNEISGLSGIDILTSA 241
Db 122 QSAFFPESGKPFKIQVLVDPDHFKVAVNDAHLOYNHRMKNLREISQLGISGIDILTSA 181
Qy 242 SYTMI 246
Db 182 NHAMI 186

RESULT 2
Q0713 PRELIMINARY; PRT; 262 AA.
AC Q0713;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Galectin-3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Gorski J.P., Liu F.-T., Artigues A., Castagna L.F., Osdoby P.;
RT "New alternatively spliced form of galectin-3, a member of beta-
galactoside-binding animal lectin family, contains predicted
transmembrane spanning domain and leucine zipper motif.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF479564; AAL91920.1;
KW Transmembrane.
SQ SEQUENCE 332 AA; 35484 MW; CF3203BC99418CB1 CRC64;

Query Match 48.9%; Score 663.5; DB 13; Length 332;
Best Local Similarity 46.5%; Pred. NO. 5.4e-50;
Matches 151; Conservative 24; Mismatches 49; Indels 101; Gaps 15;

Qy 7 LHDALSGS-----GNPNQGWPGWNGNPAGAGGYPGAYPGQAP--PGAYPGQAP 58
Db 24 LHPQLSDALPAHNPAGPPQGW-----NRPPGPGAPP--AYGYPGAYPGAGPYG--A 74
Qy 59 PGAYHGAGYCAPAGPYGPPSGGAYPSGQPSAPGAY---ATGPGY-APAGPLI- 113
Db 75 PGPHGGPGGYPGPGP-PGYPGPGP--PGYP--GGP--PGYPGPGTAPYSEAPAPLVT 127
Qy 114 -----
Db 128 ALSYFKGFCFSSSLCLAMGGTWGCVSLGCMSSHIAVMSTPCLTVRPVLLANVLFCL 187
Qy 114 -----VPYNLPLPGVVPRLITILGTVKPNANRIALDFQRNDVAFHF-PRFNEN 163
Db 188 TPNPCPLQKVPYDPLPLPAGLMPRLITITVTNSNPNRSLDFKRGQDIAFHNPRKED 247
Qy 164 NRRVIVCNTKLDNNNGREEQSV-PPFESGKPFKIQVLVDPDHFKVAVNDAH-LOYNHRV 221
Db 248 HKRVIVCNMFSQNNWKEERTAPRFPFGTPTPKLQVLCEGDFHKVAVNDAHLLOFNRE 307
Qy 222 KLINEISKLISGIDILTSASYTMI 246
Db 308 KKLNEITKLCIAGDITLTSVLTSMI 332

RESULT 4
Q61357 PRELIMINARY; PRT; 139 AA.
AC Q61357;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Beta-galactoside-binding lectin (L-34) (Fragment).
GN LGALS3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

DR MGD; MGI:96778; Lgals3.
DR InterPro: IPR001079; Galectin.
DR Pfam: PF00337; Gal_bind_lectin; 1.
DR SMART: SM00276; GLECT; 1.
DR PROSITE: PS00309; GALAPTIN; 1.
DR NON_TER 1
SQ SEQUENCE 186 AA; 19938 MW; 0971F91053126996 CRC64;

Query Match 56.6%; Score 768; DB 11; Length 186;
Best Local Similarity 80.0%; Pred. NO. 1.9e-59;
Matches 148; Conservative 11; Mismatches 18; Indels 8; Gaps 4;

Qy 65 APGAYCAPAGPYGPPSGGAYPSGQPSAPGAY-ATGPGAPAGPLIVPNLPLPG 123
Db 7 AGGAYPGSTAPGAPGPGGAPGAY-----PSAPGGTAPGYPVAGPLTVPYDPLPG 61
Qy 124 VVPRMLITILGTVKPNANRIALDFQRNDVAFHF-PRFNENRRVIVCNTKLDNNNGREE 182
Db 62 VMPRLITINGTVKPNANRIALDFQRNDVAFHFPRFNENRRVIVCNTKQDNNNGKEE 121
Qy 183 QSVFPFESGKPFKIQVLVDPDHFKVAVNDAH-LOYNHRVKKLNEISGLSGIDILTSA 241
Db 122 QSAFFPESGKPFKIQVLVDPDHFKVAVNDAHLOYNHRMKNLREISQLGISGIDILTSA 181
Qy 242 SYTMI 246
Db 182 NHAMI 186

RESULT 2
Q0713 PRELIMINARY; PRT; 262 AA.
AC Q0713;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Galectin-3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Nurninskaya M.V., Linsenmayer T.F.;
RT "Identification and characterization of up-regulated genes during
chondrocyte hypertrophy.";
RL Dev. Dyn. 0:0-0(1996).
DR EMBL: U50339; AAB02856.1;
DR HSSP: P17931; 1A3K.
DR InterPro: IPR001079; Galectin.
DR Pfam: PF00337; Gal_bind_lectin; 1.
DR SMART: SM00276; GLECT; 1.
DR PROSITE: PS00309; GALAPTIN; UNKNOWN_1.
SQ SEQUENCE 262 AA; 28155 MW; 2D89581493BBCA30 CRC64;

Query Match 51.3%; Score 695.5; DB 13; Length 262;
Best Local Similarity 58.8%; Pred. NO. 6.4e-53;
Matches 150; Conservative 23; Mismatches 51; Indels 31; Gaps 14;

Qy 7 LHDALSGS-----GNPNQGWPGWNGNPAGAGGYPGAYPSGYPGQAP--PGAYPGQAP 58
Db 24 LHPQLSDALPAHNPAGPPQGW-----NRPPGPGAPP--AYGYPGAYPGAGPYG--A 74
Qy 59 PGAYHGAGYCAPAGPYGPPSGGAYPSGQPSAPGAY---ATGPGY-APAGPLI 114
Db 75 PGPHGGPGGYPGPGP-PGYPGPGP--PGYP--GGP--PGYPGPGTAPYSEAPAPLKV 127
Qy 115 PYNLPLPGVVPRLITILGTVKPNANRIALDFQRNDVAFHF-PRFNENRRVIVCNTK 173
Db 128 PYDPLPAGLMPRLITITVTNSNPNRSLDFKRGQDIAFHNPRFKEDHKRVIVCNM 187

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RX MEDLINE=88080093; PubMed=3335026;
RA Raz A., Carmi P., Pazerini G.
RT "Expression of two different endogenous galactoside-binding lectins
RT sharing sequence homology."
RL Cancer Res. 48:645-649(1988).
DR EMBL; M33215; AAA37314.1; -.
DR HSSP; P17931; 1A3K.
DR MGD; MGI:96778; Lgals3.
DR InterPro; IPR001079; Galectin.
DR Pfam; PF00337; Gal-bind_lectin; 1.
DR SMART; SM00276; GLECT; 1.
DR PROSITE; PS00309; GALAPTIN; 1.
KW Lectin.
FT NON_TER
FT SEQUENCE 139 AA; 15914 MW; B6373F3DBC378568 CRC64;
SQ
Query Match 32.7%; Score 444; DB 11; Length 139;
Best Local Similarity 76.8%; Pred. NO. 2.7e-31;
Matches 86; Conservative 7; Mismatches 17; Indels 2; Gaps 2;
QY 104 PYGAPAGPLIVPNLPLGGVVPRLITILGTVKPNANRIALDFQGNDAVAFHF-PRFNE 162
DB 22 PLWCPRWTTVDYDPLPLGGVVPRLITILGTVKPNANRIALDFQGNDAVAFHF-PRFNE 81
QY 163 NNRRIVTCNKLNNWGREOSVFPFESGKPKIQVLVEPDHFKVAVNDAH 214
DB 82 NNRRIVTCNKLNNWGREOSVFPFESGKPKIQVLVAADHSGCG-HDAH 132
RESULT 5
Q9PT11 PRELIMINARY; PRT; 341 AA.
AC Q9PT11
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Galectin like protein.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEAD KIDNEY;
RA Soma G., Inagawa H., Honda T., Nakanishi T., Ootake M., Nishizawa T.,
RA Kanou J., Endo M.;
RT "Rainbow trout cDNA similar to galectin 9 like.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB027452; BAA88670.1; -.
DR HSSP; P47929; 1BKZ.
DR InterPro; IPR001079; Galectin.
DR Pfam; PF00337; Gal-bind_lectin; 2.
DR SMART; SM00276; GLECT; 2.
DR PROSITE; PS00309; GALAPTIN; UNKNOWN1.
SQ SEQUENCE 341 AA; 37816 MW; 176D835EC19550C4 CRC64;
Query Match 23.2%; Score 314.5; DB 13; Length 341;
Best Local Similarity 36.0%; Pred. NO. 1.7e-19;
Matches 90; Conservative 30; Mismatches 69; Indels 61; Gaps 17;
QY 9 DALSSG-----NNP-----QGWPGANGQACAGYPGASGCGYCGQAPPGAY 53
DB 132 DTSADGKVELSVIFQNPAPTIPQAQCGFPA-----QP-----GFP--SYGFPQAQ--PG-F 178
QY 54 PGQAPPGAYHGAPGAPGAPGVPGPPSGPGAYPSGQSPAPGAYATGPY-GAPAGPL 112
DB 179 P-----SYPGFPA---QGFPSFCFG-PP-CQPCF-----PYGFPQAQ-P 211

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QY 113 IVPYNLPLGGVVPRLITILGTVKPNANRIALDFQGNDAVAFHF-PRFNNRRVIVCN 171
DB 212 AVPYKNNGGLYPGRITINIQGVNPNANRFINLNFSGIALHFNPREDET---LVVRN 268
QY 172 TKLDNNWGREOSVFPFESGKPKIQVLVEPDHFKVAVNDAHQ-YNHRVKKLNEISK 230
DB 269 SKLDQWNGKEERGGMPFHRGQAFITSLTCDACQYKIVVNGNOTSTYKHKHRTLLQOVN 328
QY 231 GISGDIDLS 240
DB 329 EVDGDLSTLS 338
RESULT 6
Q99L83 PRELIMINARY; PRT; 322 AA.
AC Q99L83
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-WAR-2002 (TRENBLrel. 20, Last annotation update)
DE Lectin, galactose binding, soluble 9.
GN LGALS9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003754; AAH03754.1; -.
DR HSSP; P17931; 1A3K.
DR MGD; MGI:109496; Lgals9.
DR InterPro; IPR001079; Galectin.
DR Pfam; PF00337; Gal-bind_lectin; 2.
DR SMART; SM00276; GLECT; 2.
DR PROSITE; PS00309; GALAPTIN; 2.
SQ SEQUENCE 322 AA; 36545 MW; 032D77400737562E CRC64;
Query Match 22.0%; Score 299; DB 11; Length 322;
Best Local Similarity 37.5%; Pred. NO. 3.7e-18;
Matches 69; Conservative 28; Mismatches 47; Indels 40; Gaps 8;
QY 63 HGAPG---AYGAPAGVYVGGPGPGAYPSGQSPAPGAYATGPYCAPAGPLIVPNLP 119
DB 168 HSTPGQMFSTPGIP-PVYVTP-----AYT-----IPFYP 197
QY 120 LPGGVVPRLITILGTVKPNANRIALDFQGNDAVAFHF-PRFNNRRVIVTCNKLNNW 178
DB 198 IPNGLYPSKIMSISGNVLDPDTRFHLNRCGGDIAPHLNPRFEN---AVVRTQINNSW 254
QY 179 GREERQSV--FPFESGKPKIQVLVEPDHFKVAVNDAH--OYNHRVKKLNEISKLGISGD 235
DB 255 GQEERSLGRMPFSRCQSFVWICEGHCFKVAVNGQHMCYHRLKNLODINTLEAVGD 314
QY 236 IDIT 239
DB 315 IQLT 318
RESULT 7
Q8QGB1 PRELIMINARY; PRT; 348 AA.
AC Q8QGB1
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE VHSV-induced protein-9.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;

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RN SEQUENCE FROM N.A.
RP
RA Benmansour A., Boubinot P., Vaghefi N., O'Farrell C.;
RT "Global Survey of Transcript Expression in Rainbow Trout Leukocytes
RT Reveals a Major Contribution of Interferon Responsive Genes in the
RT Early Response to a Rhabdovirus Infection."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF483533; AAMI8472.1; -
SQ SEQUENCE 348 AA; 39054 MW; 35CA636A51478BDF CRC64;

Query Match 20.0%; Score 271; DB 13; Length 348;
Best Local Similarity 32.2%; Pred. No. 1.1e-15;
Matches 77; Conservative 34; Mismatches 108; Indels 20; Gaps 7;

QY 4 NFSLDALSGSNPNQGWPGAWGNQAGAGGYPGAGYPGGAPGAYPGGAPGAYH 63
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB 125 SFSRVDTSVGGVEVQSI--AFSN-PAVTSPPQPGYPGHP-----HSGORNRNR 174
QY 64 GAPGAYPCAPAGYVYVPGPPSGGAYPSSGQPSAPGAYATGYPGAPGLIYVYNLPLPG 123
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB 175 QSKTHQKTP-----PQNCNATQAFSAAGFLQAPPYTAQPPYTPKPSFVVPYKNIMAG 229
QY 124 VYPRMLITILGTVKPNANRIALDFQRGNDAVHF--PRFNNRRVIVCNTKLDNNWGEE 182
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB 230 LYPGRNIIQGVVHNADKFCINLRFNSGVAFHFNRENEN---VVVRNLSLLKEQWGPEE 286
QY 183 ROSVFPFESGPKFKIOVLVEPDHFKVAVNDAHL-QYNHRVKKLEISKLGISGIDLTS 240
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB 287 RTGGMFPYRGQPTVIIMCDTQCYRMVNGALMFSYNRPHFLFOQIDILEVEGDVLSA 345

RESULT 8
QYQYQ7 PRELIMINARY; PRT; 311 AA.
AC Q8WYQ7;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Galectin-9.
GN LGALS9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Akiyama S.;
RT "Homo sapiens galectin-9 (LGALS9) / ealectin gene, exon 2 through
RT 11."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB040130; BAB83623.1; -.
DR EMBL; AB040129; BAB83623.1; JOINED.
DR InterPro; IPR001079; Galectin.
DR Pfam; PF00337; Gal-bind_lectin; 2.
DR SMART; SM00276; GLECT; 2.
DR PROSITE; PS00309; GALAPTIN; UNKNOWN_2.
SQ SEQUENCE 311 AA; 34690 MW; 3D00232FE39D776C CRC64;

Query Match 19.5%; Score 264; DB 4; Length 311;
Best Local Similarity 36.5%; Pred. No. 4e-15;
Matches 66; Conservative 25; Mismatches 52; Indels 38; Gaps 7;

QY 65 APGAYPCAPA--PGVYPPGPGGAYPSSGQPSAPGAYATGYPGAPGLIYVYNLPLPG 122
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB 159 APQMFETPAIPMYPH-----AYP-----MPFITILG 189
QY 123 GVPRMLITILGTVKPNANRIALDFQRGNDAVHF--PRFNNRRVIVCNTKLDNNWGEE 181
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB 190 GLYPSKILLSGLVPLSAQRFHNLCSGNHIAFLNPRFEN---AVVRNTQIDNSWGE 246
QY 182 ERQ--SVYFPFESGPKFKIOVLVEPDHFKVAVNDAHL-QYNHRVKKLEISKLGISGIDL 238
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB 247 ERSIPKMPFVRGQSFVSWILCEAHCLKVAVDQHLFEYHRLNRLPTINRLEVGDIQL 306

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QY 239 T 239
DB 307 T 307

RESULT 9
QYQSM9 PRELIMINARY; PRT; 349 AA.
AC Q9XSM9;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Urate transporter/channel protein, isoform (UATp,1).
GN UATP.1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Spitzberger F., Graessler J., Schroeder H.E.;
RT "Molecular characterization and functional expression of a renal urate
RT transporter/channel from cultured LLC-PK1 epithelial cells."
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ131827; CAB44279.1; -.
DR HSSP; PI7931; 1A3K.
DR InterPro; IPR001079; Galectin.
DR Pfam; PF00337; Gal-bind_lectin; 2.
DR SMART; SM00276; GLECT; 2.
DR PROSITE; PS00309; GALAPTIN; 1.
SQ SEQUENCE 349 AA; 38899 MW; BF83D3E213E7B64C CRC64;

Query Match 19.2%; Score 260; DB 6; Length 349;
Best Local Similarity 31.7%; Pred. No. 1e-14;
Matches 66; Conservative 32; Mismatches 68; Indels 42; Gaps 9;

QY 37 PGASYPGYPGQ--APGAYPGQAPP-----GAYHGAPGAYPCAPGAYVYPPGPGAY 88
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB 167 PACFPFRHKRKPGRWPNASAPITQTVIHTVQSTPGQ-----MFPNPMIPPMAY 218
QY 89 PSSQPSAPGAYATGYPGAPGLIYVYNLPLPGVVPVPRMLITILGTVKPNANRIALDFQ 148
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB 219 PN-----PVFP--IPFFASIPGGLYPSKSIWVSGTILPSAQSFYNLR 259
QY 149 RGNDAVHF--PRFNNRRVIVCNTKLDNNWGEE--QSVFFESGPKFKIOVLVEPDH 205
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB 260 SGSDIAFLNPRFEN---AVVRNTQIGSSWGPEERGLPRKMPFSRQGSFLVWLCSHC 316
QY 206 FKVAVNDAHL-QYNHRVKKLEISKLGI 232
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB 317 FKVAVDQHLFEYHRLKHLPTINSLEV 344

RESULT 10
QYQSM9 PRELIMINARY; PRT; 343 AA.
AC Q8UW98;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Galectin family xgalectin-IIIa.
GN XGALECTIN-IIIa.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Shoji H., Nishii N., Hirashima M., Nakamura T.;

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RP SEQUENCE FROM N.A.
RC TISSUE-COLON;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-COLON;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011236; AAH11236.1; -
DR EMBL; BC021632; AAH21632.1; -
DR MGD; MGI:107536; Igals4.
DR InterPro; IPR001079; Galectin.
DR Pfam; PF00337; Gal-bind_lectin; 2.
DR PROSITE; PS00309; GALAPTIN; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 326 AA; 36372 MW; 7F3DD89862A853B5 CRC64;
Query Match 17.9%; Score 243.5; DB 11; Length 326;
Best Local Similarity 35.8%; Pred. No. 2.6e-13;
Matches 54; Conservative 31; Mismatches 57; Indels 9; Gaps 5;
QY 99 AYATGPGYAGAPGLIVPNLPLPGVVPRLITILGTVPKNANRIALDF---QRGNDVA 154
DB 2 AYPAPGYQPTYNLTLPKPIPGGLSVGMSVYIQGMKMRFRHVFVAVGQDDGADVA 61
QY 155 FHF-PREFNENRRVIVCNTKLDNNWGREERQSVFPFSGKPKIQVLVEPDHFKVAVN-D 212
DB 62 FHFNPREDGMDK--VFNTQSGQGWGKEKKKSPFQKHFLVFMVMEHYKVVVNGN 119
QY 213 AHLYQNRHVKKLNEISKLGISGDDILTSASY 243
DB 120 SFYEYGHRL-PVQMVTHLQVDGDLQSLINF 149
RESULT 14
Q9TUB8 PRELIMINARY; PRT; 328 AA.
ID Q9TUB8
AC Q9TUB8;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Galectin-4.
GN LGALS4.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NEW ENGLAND WHITE;
RX MEDLINE=20147388; PubMed=10683764;
RA Jiang W., Puch S., Guo X., Bhavanandan V.P.;
RT "Signature sequences for the galectin-4 subfamily."
RL IUBMB Life 48:601-605(1999).
DR EMBL; AF091738; AAD55242.1; -
DR HSP; P47929; LBKZ.
DR InterPro; IPR001079; Galectin.
DR Pfam; PF00337; Gal-bind_lectin; 2.
DR SMART; SM00276; GLECT. 2.
DR PROSITE; PS00309; GALAPTIN; UNKNOWN_2.
SQ SEQUENCE 328 AA; 36462 MW; 030BFF1B723D2ACF CRC64;
Query Match 17.2%; Score 233.5; DB 6; Length 328;
Best Local Similarity 34.5%; Pred. No. 2e-12;
Matches 68; Conservative 23; Mismatches 81; Indels 25; Gaps 10;
QY 55 GQAPPGAYHGAPGAPGAPGVTPGPGPSSGQSPAPGAYATGYPGAPGLIV 114
DB 152 GQPTP---HQRPWTTPGYPSPGY--GHP-GYGAQPLHSLPSMEGPTFNP-----PV 197
QY 115 PYNLPLPGVVPRLITILGTVPKNANRIALDFQGN--DVAFHF-PREFNENRRVIVCN 171

DB 198 PFTGRLOGLTARTTIIVKGYVPTGKSFINKFVSSGDLALHINPRMTEG---VVVRN 254
QY 172 TKLDNNWGREERQSVF-PFESGKPKIQVLVEPDHFKVAVNDAHL-QYNRHVKKLNEISK 229
DB 255 SRLNGSWGAERKWAYNPFPGQYFDLSIRCGMDRKFYANGQHLFDYAHREFAFQKVDV 314
QY 230 LGISGDDILTSASYTMI 246
DB 315 IEIQGDVAL---SYVQI 328
RESULT 15
Q8TEV1 PRELIMINARY; PRT; 359 AA.
ID Q8TEV1
AC Q8TEV1;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Lymphocyte/NHL galectin-8 long isoform.
GN LGALS8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Moisan S., Mercier J., Demers M., Belanger S.D., Alain T.,
RA Kossakowska A.E., Potworowski E.F., St-Pierre Y.;
RT "Galectins in murine and human non-Hodgkin's lymphomas";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF468213; AAL77076.1; -
SQ SEQUENCE 359 AA; 40151 MW; F87BFE92E46F571 CRC64;
Query Match 16.8%; Score 228.5; DB 4; Length 359;
Best Local Similarity 40.0%; Pred. No. 6.1e-12;
Matches 56; Conservative 22; Mismatches 51; Indels 11; Gaps 5;
QY 113 IVYPNPLPGVVPRLITILGTVPKNANRIALDFQGN-----DVAFHF-PREFNENNR 165
DB 16 VIPYVGTIPQLDPGTLIVICGHVPSDADRFDQVLDQNGSSVKPRADYAFHFNPRFKRAG- 74
QY 166 RVIVCNTKLDNNWGREERQSVFPFESGKPKIQVLVEPDHFKVAVNDAH-LQYNHRVKKL 224
DB 75 -CIVCNTLINEKMGREITTYDTPFKREKSEFIVIMVLKDFQVAVNGKHTLLYGHRIGP- 132
QY 225 NEISKLGISGDDILTSASYT 244
DB 133 EKIDTLGIYGVNLSIGFS 152
Search completed: May 20, 2003, 12:19:34
Job time : 36 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: May 20, 2003, 12:18:00 ; Search time 30 Seconds
(without alignments)
241.268 Million cell updates/sec

Title: US-09-297-040-4
Perfect score: 1357
Sequence: 1 MADNFSLHDLSCGNPNQ.....ISKLGISGIDILTSASYTMI 246

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
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3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1315	96.9	250	3	US-08-946-914-10
2	1315	96.9	250	4	US-09-656-450-10
3	1305	96.2	250	1	US-08-562-311-2
4	1079	79.5	262	3	US-08-946-914-14
5	1079	79.5	262	4	US-09-656-450-14
6	1078	79.4	264	1	US-08-562-311-4
7	513	37.8	135	2	US-08-647-960-5
8	264	19.5	311	3	US-08-946-914-4
9	264	19.5	311	4	US-09-656-450-4
10	250.5	18.5	145	2	US-08-788-584-5
11	250.5	18.5	145	3	US-08-946-914-12
12	250.5	18.5	145	4	US-09-656-450-12
13	249	18.3	149	2	US-08-788-584-3
14	243.5	17.9	145	2	US-08-788-584-1
15	236.5	17.4	324	3	US-08-946-914-11
16	236.5	17.4	324	4	US-09-656-450-11
17	223.5	16.5	200	3	US-08-946-914-8
18	223.5	16.5	200	4	US-09-656-450-8
19	223.5	16.5	316	4	US-09-131-648-5
20	223.5	16.5	317	3	US-08-946-914-6
21	223.5	16.5	317	4	US-09-656-450-6
22	218.5	16.1	316	2	US-08-728-521-3
23	218.5	16.1	316	2	US-08-647-960-2
24	218.5	16.1	316	3	US-08-946-914-15
25	218.5	16.1	316	3	US-08-946-914-17
26	218.5	16.1	316	4	US-09-212-146-3
27	218.5	16.1	316	4	US-09-656-450-15

28	218.5	16.1	316	4	US-09-656-450-17	Sequence 17, Appl
29	215.5	15.9	323	1	US-08-469-667-16	Sequence 16, Appl
30	215.5	15.9	323	3	US-08-946-914-2	Sequence 2, Appl
31	215.5	15.9	323	4	US-09-224-110-16	Sequence 2, Appl
32	215.5	15.9	323	4	US-09-656-450-2	Sequence 2, Appl
33	215.5	15.9	323	5	PCT-US95-07289-16	Sequence 16, Appl
34	211	15.5	136	3	US-08-946-914-13	Sequence 13, Appl
35	211	15.5	136	4	US-09-154-750A-79	Sequence 79, Appl
36	211	15.5	136	4	US-09-656-450-13	Sequence 13, Appl
37	200.5	14.8	504	4	US-09-219-849-3	Sequence 3, Appl
38	200.5	14.8	561	1	US-08-642-255-52	Sequence 52, Appl
39	199.5	14.7	144	1	US-08-642-255-49	Sequence 49, Appl
40	199.5	14.7	720	4	US-09-219-849-4	Sequence 4, Appl
41	199.5	14.7	777	1	US-08-642-255-53	Sequence 53, Appl
42	197.5	14.6	234	1	US-08-642-255-51	Sequence 51, Appl
43	196.5	14.5	466	3	US-08-526-136-13	Sequence 13, Appl
44	195.5	14.4	417	1	US-08-175-155-69	Sequence 69, Appl
45	195.5	14.4	417	1	US-08-477-509B-104	Sequence 104, App

ALIGNMENTS

RESULT 1
US-08-946-914-10
; Sequence 10, Application US/08946914
; Patent No. 6027916
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Galectin 8, 9, 10 and 10SV
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein, & Fox P.L.L.C.
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/946,914
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,093
; FILING DATE: 09-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0560001/EKS/SGW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 250 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-946-914-10

Query Match 96.9%; Score 1315; DB 3; Length 250;
Best Local Similarity 98.4%; Pred. No. 1.8e-114;
Matches 246; Conservative 0; Mismatches 0; Indels 4; Gaps 4;
QY 1 MADNFSLHDLSCGNPNQGWPGWAGNQAGAGGYGASYPG-YPCQAPPAYPCQAPP 59

|||||
Db 1 MADNFSLHDALSGGNPNQGWPGANGNPAGAGGYPGASYPGAYPGQAPP 60
QY 60 GAYHAGPAGPAGPAGVPGPPSGPAGYSSQPSAPGAY-ATGPGAPAGPLIYPYNL 118
Db 61 GAYHAGPAGPAGPAGVPGPPSGPAGYSSQPSAPGAYPATGPGAPAGPLIYPYNL 120
QY 119 PLPGGVVPRMLITILGTGVPKPNANRIALDFQGNDAFHF-PRFNNRRVIVCNTKLDNN 177
Db 121 PLPGGVVPRMLITILGTGVPKPNANRIALDFQGNDAFHFPRFNNRRVIVCNTKLDNN 180
QY 178 WGREERQSVFPFESGKPKFQVLVEPDHFKVAVNDAH-LOYNHRVKKLNEISKLGISGDI 236
Db 181 WGREERQSVFPFESGKPKFQVLVEPDHFKVAVNDAHLLQYNHRVKKLNEISKLGISGDI 240
QY 237 DLTSASYTMI 246
Db 241 DLTSASYTMI 250

RESULT 2
US-09-656-450-10
; Sequence 10, Application US/09656450
; Patent No. 6468768
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Galectin 9 and 10SV Polynucleotides
; FILE REFERENCE: 1488.0560003
; CURRENT APPLICATION NUMBER: US/09/656,450
; CURRENT FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 09/263,689
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: US 08/946,914
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: US 60/028,093
; PRIOR FILING DATE: 1996-10-09
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 10
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-656-450-10

Query Match 96.98; Score 1315; DB 4; Length 250;
Best Local Similarity 98.48; Pred. No. 1.8e-114;
Matches 246; Conservative 0; Mismatches 0; Indels 4; Gaps 4;
QY 1 MADNFSLHDALSGGNPNQGWPGANGNPAGAGGYPGASYPG-YPGQAPP 59
Db 1 MADNFSLHDALSGGNPNQGWPGANGNPAGAGGYPGASYPGAYPGQAPP 60
QY 60 GAYHAGPAGPAGPAGVPGPPSGPAGYSSQPSAPGAY-ATGPGAPAGPLIYPYNL 118
Db 61 GAYHAGPAGPAGPAGVPGPPSGPAGYSSQPSAPGAYPATGPGAPAGPLIYPYNL 120
QY 119 PLPGGVVPRMLITILGTGVPKPNANRIALDFQGNDAFHF-PRFNNRRVIVCNTKLDNN 177
Db 121 PLPGGVVPRMLITILGTGVPKPNANRIALDFQGNDAFHFPRFNNRRVIVCNTKLDNN 180
QY 178 WGREERQSVFPFESGKPKFQVLVEPDHFKVAVNDAH-LOYNHRVKKLNEISKLGISGDI 236
Db 181 WGREERQSVFPFESGKPKFQVLVEPDHFKVAVNDAHLLQYNHRVKKLNEISKLGISGDI 240
QY 237 DLTSASYTMI 246
Db 241 DLTSASYTMI 250
RESULT 3
US-08-946-914-12

; Sequence 2, Application US/08562311
; Patent No. 5801002
; GENERAL INFORMATION:
; APPLICANT: RAZ, AVRAHAM
; TITLE OF INVENTION: A METHOD OF DETERMINING THE PROBABILITY
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dykema Gossett
; STREET: STE 505 N. Woodward
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: U.S.
; ZIP: 48304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/562,311
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,225
; FILING DATE:
; APPLICATION NUMBER: US 07/681,242
; FILING DATE: 04-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/294,249
; FILING DATE: 01-JUN-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: KELLY, ROBERT L.
; REGISTRATION NUMBER: 31,843
; REFERENCE/DOCKET NUMBER: 61,686-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 810-540-0849
; TELEFAX: 810-540-0763
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 250 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-562-311-2

Query Match 96.2%; Score 1305; DB 1; Length 250;
Best Local Similarity 97.6%; Pred. No. 1.5e-113;
Matches 244; Conservative 0; Mismatches 2; Indels 4; Gaps 4;
QY 1 MADNFSLHDALSGGNPNQGWPGANGNPAGAGGYPGASYPG-YPGQAPP 59
Db 1 MADNFSLHDALSGGNPNQGWPGANGNPAGAGGYPGASYPGAYPGQAPP 60
QY 60 GAYHAGPAGPAGPAGVPGPPSGPAGYSSQPSAPGAY-ATGPGAPAGPLIYPYNL 118
Db 61 GAYHAGPAGPAGPAGVPGPPSGPAGYSSQPSAPGAYPATGPGAPAGPLIYPYNL 120
QY 119 PLPGGVVPRMLITILGTGVPKPNANRIALDFQGNDAFHF-PRFNNRRVIVCNTKLDNN 177
Db 121 PLPGGVVPRMLITILGTGVPKPNANRIALDFQGNDAFHFPRFNNRRVIVCNTKLDNN 180
QY 178 WGREERQSVFPFESGKPKFQVLVEPDHFKVAVNDAH-LOYNHRVKKLNEISKLGISGDI 236
Db 181 WGREERQSVFPFESGKPKFQVLVEPDHFKVAVNDAHLLQYNHRVKKLNEISKLGISGDI 240
QY 237 DLTSASYTMI 246
Db 241 DLTSASYTMI 250
RESULT 4
US-08-946-914-14

FILING DATE: 04-APR-1991
APPLICATION NUMBER: US 07/681,242
FILING DATE: 04-APR-1991
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER: US 07/294,249
FILING DATE: 01-JUN-1989
ATTORNEY/AGENT INFORMATION:
NAME: KELLY, ROBERT L.
REGISTRATION NUMBER: 31,843
REFERENCE/DOCKET NUMBER: 61,686-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 810-540-0849
TELEFAX: 810-540-0763
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 264 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-562-311-4

Query Match 79.4%; Score 1078; DB 1; Length 264;
Best Local Similarity 78.2%; Pred. No. 1.8e-92;
Matches 208; Conservative 15; Mismatches 21; Indels 22; Gaps 8;

QY 1 MADNFSLHDALSGSGNPNPQGWGPNAGAGGTPGASYPG-YGQAPPGAYPGQAPP 59
DB 1 MADTFLSNDALAGSGNPNPQGYPGAWGNP-GAGGYPGAAYPGAYPGQAPPAYPGQAPP 59
QY 60 GAYHG--APGAYPGAPAGPVYPPSGPGAGPSS-----GQSPAPGAY-----AT 102
DB 60 GAYPGQAPSPAYPGPTACAYPG-PTAPGAYPGSTAGPFGQPGAGPAGPSPAGGYPAA 118
QY 103 GPYGAPAGLIYPIYNLPPLPGGVVPRMLITLGTVKPNANRIALDFRGNDVAFHF-PRN 161
DB 119 GPYGVPGAGPLTPYDLPPLPGGLMPRLITIMGTVKPNANRIVLDFRGNDVAFHFPRN 178
QY 162 ENNRVIVCNTKLDNNWGEREQSVFPEESKPKFIQVLVEPDHFKVAVNDAH-LQYNHR 220
DB 179 ENNRVIVCNTKQDNNWKEERQSNFPEESKPKFIQVLVEADHFKVAVNDAHLQYNHR 238
QY 221 VKKLEISKLGISGDDILTSASYTI 246
DB 239 MKNLEISQLGISGDDILTLSANHAM 264

RESULT 7
US-08-647-960-5
Sequence 5, Application US/08647960
Patent No. 5908761
GENERAL INFORMATION:
APPLICANT: ZICK, Vehiel
TITLE OF INVENTION: GALECTIN-8 AND GALECTIN-8-LIKE PROTEINS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/647,960
FILING DATE: 30-MAY-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107860
FILING DATE: 05-DEC-1993

RESULT 10

; TITLE OF INVENTION: Galactin 8, 9, 10 and 10SV
 ; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sterne, Kessler, Goldstein, & Fox P.L.L.C.
 ; STREET: 1100 New York Ave., Suite 600
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/946,914
 ; FILING DATE: Herewith
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/028,093
 ; FILING DATE: 09-OCT-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Steffe, Eric K.
 ; REGISTRATION NUMBER: 36,688
 ; REFERENCE/DOCKET NUMBER: 1488.0560001/EKS/SGW
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-2600
 ; TELEFAX: 202-371-2540
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 145 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: CDNA
 ; US-08-946-914-12

Query Match 18.5%; Score 250.5; DB 3; Length 145;
Best Local Similarity 40.4%; Pred. NO. 4.8e-16;
Matches 55; Conservative 26; Mismatches 48; Indels 7

[illegible]

```

RESULT 12
US-09-656-450-12
; Sequence 12, Application US/09656450
; Patent No. 6468768
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Galectin 9 and 10SV Polynucleotides
; FILE REFERENCE: 1488.0560003
; CURRENT APPLICATION NUMBER: US/09/656,450
; CURRENT FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 09/263,689
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: US 08/946,914
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: US 60/028,093
; PRIOR FILING DATE: 1996-10-09
; NUMBER OF SEQ ID NOS: 60

```

12

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Rat
US-09-656-450-12

```

Query Match	18.5%	Score 250.5;	DB 4;	Length 145;
Best Local Similarity	40.4%	Pred. No. 4.8e-16;		
Matches	55; Conservative	26; Mismatches	48; Indels	7

Qy . 108 PAGGLIVPNLPLGGVWPRMLITILGTVPKANRIALDFQRNDVAHF-PRFENNRR 166
| | | : : : | | | : : : | | : : | | : : ||
Db 9 PYPNLAVPFTSIPNGLYPSKSIVISGWLSDAKRFQINLCGGDIAFHLPREFDEN--- 65

Qy	167	VIVCNTKLDNNWGRERQ--SVFPFESGKPFKIQLVLVEDPHFKVAVNDAHL-QYNHRVKK	223
Db	66	AVYRNTQINNSWGPPERSLPGSMPPFRGQRFSWILCEGHCFKVAVDGOHICEYSRLMN	125

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QY      224 LNEISKLISGDIDLT 239
          | : | : | : | : |
Db      126 LPDINTLEVAGDIQLT 141
```

RESULT 13
US-08-788-584-3
Sequence 3, Application US/08788584
Patent NO. 5837493
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Phillip R.
APPLICANT: Petithory, Joanne R.
TITLE OF INVENTION: NOVEL HUMAN GALECTINS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA

```

, ZIP: 94304
,
, COMPUTER READABLE FORM:
,
, MEDIUM TYPE: Diskette
,
, COMPUTER: IBM Compatible
,
, OPERATING SYSTEM: DOS
,
, SOFTWARE: FASTSEQ for Windows Version 2.0
,
, CURRENT APPLICATION DATA:
,
, APPLICATION NUMBER: US/08/788,584
,
, FILING DATE: Filled Herewith
,
, CLASSIFICATION: 436
,
, PRIOR APPLICATION DATA:
,
, APPLICATION NUMBER:
,
, FILING DATE:
,
, ATTORNEY/AGENT INFORMATION:
,
, NAME: Billings, Lucy J.
,
, REGISTRATION NUMBER: 36,749
,
, REFERENCE/DOCKET NUMBER: PF-0192 US
,
, TELECOMMUNICATION INFORMATION:
,
, TELEPHONE: 415-855-0555
,
, TELEFAX: 415-845-4166
,
, INFORMATION FOR SEQ ID NO: 3:
,
, SEQUENCE CHARACTERISTICS:
,
, LENGTH: 149 amino acids
,
, TYPE: amino acid
,
, STRANDEDNESS: single
,
, TOPOLOGY: linear
,
, US-08-788-584-3

```

Query Match 18.3%; Score 249; DB 2; Length 149;
Best Local Similarity 37.1%; Pred. No. 6.8e-16;
Matches 59; Conservative 23; Mismatches 51; Indels

Query Match 18.3%; Score 249; DB 2; Length 149;
Best Local Similarity 37.1%; Pred. NO. 6.8e-16;
Matches 59; Conservative 23; Mismatches 51; Indels 26; Gaps 5

	Query Match	17.98;	Score 243.5;	DB 2;	Length 145;
	Best Local Similarity	40.08;	Pred. No. 2.le-15;		
	Matches	56;	Conservative 23;	Mismatches 50;	Indels 11; Gaps 5;
Qy	104	PYGAPAGLIVPYNLPLPGGVVPRMLITILCTVFPNANRIALDFQRGNDAVAFHF-PRFNE	162		
		:	:	:	:
Db	9	PYLSPX-----VPFGSTXGGGLYPSKILLSGTVLPSAQRFHINLCSGNHGIFHLNPRFE	64		
		:	:	:	:
Qy	163	NNRRVIVCTKLDNNWGEEQQ--SVRFPEGSGKPFKIQVLVEPDHFKVAVDAHL-QVNH	219		
		:	:	:	:
Db	65	N---AVVRNNQIDKNXGSEERSLRPFKMPFVRGGSFVWILCEAHLCKVAVDQHLFEYH	121		
		:	:	:	:
Qy	220	RVKLNIEISKLGISGDIDL	239		

GenCore version 5.1.4_p5.4578
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OM protein - protein search, using sw model

Run on: May 20, 2003, 12:14:40 ; Search time 35 Seconds
(without alignments)
936.562 Million cell updates/sec

Title: US-09-297-040-4
Perfect score: 1357
Sequence: 1 MANFSLHLDALSGNPNPO.....ISKLIGSGIDILTSASVTMI 246

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1357	100.0	246	19 AAW61955	Human galectin am1
2	1315	96.9	250	23 AAU97819	Human cell membran
3	1305	96.2	250	19 AAW71218	Beta-D-galactoside
4	1305	96.2	250	23 AAU97818	Human cell membran
5	1297	95.6	250	23 AAU97816	Human cell membran
6	1297	95.6	250	23 AAU97817	Human cell membran
7	1297	95.6	250	23 AAU97820	Human cell membran
8	1297	95.6	277	22 AAG75013	Human colon cancer
9	1194	88.0	248	12 AAR12532	Human Macrophage C
10	1082	79.7	264	12 AAR12531	Mac2.16 expression

11	1082	79.7	278	12 AAR13338	Mac-2 protein incl
12	1079	79.5	262	23 AAU97821	Rat cell membrane
13	1078	79.4	264	19 AAW71219	Beta-D-galactoside
14	1075	79.2	262	13 AAR42200	IGF binding protei
15	1064.5	78.4	263	23 AAU97822	Mouse cell membran
16	1060	78.1	258	19 AAW61954	Rat galectin amino
17	593	43.7	138	7 AAP60534	C-terminal of IGF-
18	314.5	23.2	341	22 AAB97171	Rainbow trout gale
19	289	21.3	355	20 AAW85664	Galectin-9 like pr
20	289	21.3	355	20 AAY06997	Galectin-9 protein
21	289	21.3	355	23 ABB77852	Amino acid sequenc
22	289	21.3	378	22 AAE13847	Human lung tumour-
23	283	20.9	323	21 AAY56802	Human eosinophil c
24	283	20.9	323	23 ABB77853	Amino acid sequenc
25	283	20.9	323	23 ABB77853	Human NF-kB activa
26	282	20.8	329	23 AAU97036	Human bladder canc
27	264	19.5	311	19 AAW56504	Human galectin 9.
28	264	19.5	311	23 ABB77854	Amino acid sequenc
29	249	18.3	149	19 AAW61614	Human galectin GAL
30	246.5	18.2	168	21 AAB11899	Human colon tumour
31	246.5	18.2	168	22 AAM24496	Colon tumour relat
32	245.5	18.1	215	22 AAB85033	Protein encoded by
33	243.5	17.9	145	19 AAW61613	Human galectin GAL
34	228.5	16.8	316	21 AAY87403	Human PCTA-1 splic
35	228.5	16.8	316	22 AAB85030	Protein encoded by
36	228.5	16.8	358	21 AAY87404	Human PCTA-1 splic
37	228.5	16.8	358	22 AAB85031	Protein encoded by
38	228.5	16.8	368	21 AAY87405	Human PCTA-1 splic
39	228.5	16.8	368	22 AAB85032	Protein encoded by
40	225.5	16.6	351	22 AAG73728	Human colon cancer
41	223.5	16.5	200	19 AAW56506	Human galectin 10
42	223.5	16.5	317	17 AAW03519	Prostate carcinoma
43	223.5	16.5	317	19 AAW56505	Human galectin 10.
44	218.5	16.1	316	16 AAR75702	Rat galectin-8. R
45	215.5	15.9	323	18 AAW11841	Human galectin-4-1

ALIGNMENTS

RESULT 1				
AAW61955				
ID	AAW61955	standard; protein: 246 AA.		
AC	AAW61955;			
XX				
DT	18-SEP-1998	(first entry)		
XX				
DE	Human galectin amino acid sequence.			
XX				
KW	Mortalin; galectin; diabetes-mediating protein; insulin; DMP;			
KW	diabetes; drug screening assay.			
OS	Homo sapiens.			
XX				
PN	WO9820124-A2.			
XX				
PD	14-MAY-1998.			
XX				
PF	24-OCT-1997;	97WO-IB01627.		
XX				
PR	18-JUL-1997;	97US-0897098.		
PR	25-OCT-1996;	96US-0029324.		
PR	05-NOV-1996;	96US-0030088.		
PR	05-NOV-1996;	96US-0030186.		
XX				
PA	(ANDE//)	ANDERSEN H U.		
PA	(CHRI//)	BJERRE CHRISTENSEN U.		
PA	(FEYS//)	FEY S J.		
PA	(KARL//)	KARLSEN A E.		
PA	(LARS//)	MOSE LARSEN P.		
PA	(NERU//)	NERUP J.		
PA	(POCI//)	POCIOT F.		

XX
PI Andersen HU, Bjerre CHRISTENSEN U, Fey SJ, Karlsen AE;
PI Mose LARSEN P, Nerup J, Pociot F;
XX
XX WPI; 1998-286940/25.
XX
XX Identification of diabetes-mediating protein(s) - by transplanting
PT insulin-secreting cells into host at risk of developing diabetes and
PT analysing protein expression in transplanted cells
XX
XX Example 5; Fig 5; 154pp; English.
XX
XX This represents the amino acid sequence of murine mortalin. This is a
CC diabetes-mediating protective protein used in the method of invention.
CC The invention provides methods for in vivo identification of a diabetes-
CC mediating protein (DMP) by transplanting insulin-secreting cells into
CC host at risk of developing diabetes and analysing protein expression in
CC transplanted cells. The DMPs are useful in drug screening assays for
CC identifying compounds capable of modulating the development of diabetes,
CC useful as therapeutic agents for the treatment or prevention of diabetes,
CC and useful as targets of therapeutic agents capable of preventing or
CC ameliorating diabetes by modulating the expression of the DMP. Changes in
CC the expression of specific DMPs is diagnostically useful as indicator of
CC the development of diabetes.
XX
XX Sequence 246 AA;
XX
Query Match 100.0%; Score 1357; DB 19; Length 246;
Best Local Similarity 100.0%; Pred. No. 5.9e-100;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MADNFSLHDLALSGSGNPNQGWPGAWGNQAGAGYFGASYPGQAPPGAYPGQAPP 60
Db 1 MADNFSLHDLALSGSGNPNQGWPGAWGNQAGAGYFGASYPGQAPPGAYPGQAPP 60
QY 61 AYHGAPGAYGAPAGYPPGPGGAYPSSGQPSAPGAYATGYPGAPAGPLIVYNLPL 120
Db 61 AYHGAPGAYGAPAGYPPGPGGAYPSSGQPSAPGAYATGYPGAPAGPLIVYNLPL 120
QY 121 PGVVPRLITILGTVPKNANRIALDFQGNDAVFHFRFNNRRNVIVCNKLDNNWGR 180
Db 121 PGVVPRLITILGTVPKNANRIALDFQGNDAVFHFRFNNRRNVIVCNKLDNNWGR 180
QY 181 EERQSVFPFSGKPKIQVLVEPDHFKVAVNDAHLOYNHRVKKLNKLSKIGISGDI 240
Db 181 EERQSVFPFSGKPKIQVLVEPDHFKVAVNDAHLOYNHRVKKLNKLSKIGISGDI 240
QY 241 ASYTM 246
Db 241 ASYTM 246
RESULT 2
AAU97819
ID AAU97819 standard; Protein; 250 AA.
XX
AC AAU97819;
XX
XX 27-AUG-2002 (first entry)
XX
XX Human cell membrane anchor protein galectin-3 #4.
XX
XX Galectin-3; cell membrane anchor protein; Ras; antisense technology;
KW farnesylated isoform; H-Ras; K-Ras 4A; K-Ras 4B; N-Ras;
KW mitosis disorder; cancer; non-malignancy; autoimmune disease;
KW type 1 diabetes; lupus; multiple sclerosis; cirrhosis; graft rejection;
KW atherosclerosis; polycystic kidney; post-angioplasty restenosis;
KW cytostatic; immunosuppressive; antidiabetic; antiatherosclerotic;
KW neuroprotective; vasotropic; hepatotropic; human.
XX
XX Homo sapiens.
XX
XX WO200229031-A2.
PN

XX
PD 11-APR-2002.
XX
PF 01-OCT-2001; 2001WO-IL00918.
XX
XX 04-OCT-2000; 2000US-237858P.
XX
XX (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
XX
XX Kloog Y, Haklai R, Paz A, El Ad-Sfadia G, Ballan E;
XX
XX WPI; 2002-435333/46.
XX
XX Identifying anchor proteins that bind Ras protein, by producing
PT complexes of Ras and cell membrane proteins in the presence and absence
PT of a Ras antagonist and identifying a complex disrupted by the Ras
PT antagonist
XX
XX Disclosure; Page 13; 62pp; English.
XX
XX The invention describes a method of identifying cell membrane anchor
CC proteins that bind a Ras protein, involving preparing 2 reaction mixtures
CC where one mixture has a Ras antagonist. A cross linking agent is added,
CC and complexes between Ras protein and other proteins are produced. The
CC complexes are then separated and the proteins binding to Ras are
CC identified. The invention also describes a method useful for identifying
CC drug candidates that inhibit aberrant Ras activity. An antisense compound
CC comprising at least one phosphorothioate-modified nucleotide is useful
CC for disrupting aberrant Ras activity in vivo, by infusing the antisense
CC compound into a patient exhibiting this problem. The method is also
CC useful for identifying anchor proteins for the farnesylated isoforms of
CC H-Ras, K-Ras 4A, K-Ras 4B and N-Ras, whose mutated forms are known to be
CC oncogenic. Reducing or inhibiting aberrant Ras activity in vivo is useful
CC for treating diseases characterised by uncontrolled mitosis, including
CC cancers and various non-malignancies such as autoimmune disease (e.g.
CC type 1 diabetes, lupus and multiple sclerosis), cirrhosis, graft
CC rejection, atherosclerosis, polycystic kidneys and post-angioplasty
CC restenosis. This sequence encodes a galectin-3, a cell-membrane anchor
CC protein that binds an isoform of Ras.
XX
XX Sequence 250 AA;
XX
Query Match 96.9%; Score 1315; DB 23; Length 250;
Best Local Similarity 98.4%; Pred. No. 1.3e-96;
Matches 246; Conservative 0; Mismatches 0; Indels 4; Gaps 4;
QY 1 MADNFSLHDLALSGSGNPNQGWPGAWGNQAGAGYFGASYPGQAPPGAYPGQAPP 59
Db 1 MADNFSLHDLALSGSGNPNQGWPGAWGNQAGAGYFGASYPGQAPPGAYPGQAPP 60
QY 60 GAYHGAPGAYGAPAGYPPGPGGAYPSSGQPSAPGAY-ATGYPGAPAGPLIVYNL 118
Db 61 GAYHGAPGAYGAPAGYPPGPGGAYPSSGQPSAPGAYATGYPGAPAGPLIVYNL 120
QY 119 PLPGGVVPRMLITILGTVPKNANRIALDFQGNDAVFHFRFNNRRNVIVCNKLDNN 177
Db 121 PLPGGVVPRMLITILGTVPKNANRIALDFQGNDAVFHFRFNNRRNVIVCNKLDNN 180
QY 178 WGREERQSVFPFSGKPKIQVLVEPDHFKVAVNDAH-LOYNHRVKKLNKLSKIGISGDI 236
Db 181 WGREERQSVFPFSGKPKIQVLVEPDHFKVAVNDAHLOYNHRVKKLNKLSKIGISGDI 240
QY 237 DLTSASYTMI 246
Db 241 DLTSASYTMI 250
RESULT 3
AAW71218
ID AAW71218 standard; Protein; 250 AA.
XX
XX AAW71218;
XX

DT 30-OCT-1998 (first entry)
 DE Beta-D-galactoside-binding protein designated L-31-gal-lectin.
 XX
 KW Beta-D-galactoside-binding protein; L-31-gal-lectin;
 KW metastatic potential; antibody.
 XX
 OS Homo sapiens.
 XX
 PN US5801002-A.
 XX
 PD 01-SEP-1998.
 XX
 PF 22-NOV-1995; 95US-0562311.
 XX
 PR 26-JAN-1994; 94US-0188225.
 PR 06-JAN-1989; 89US-0294249.
 PR 05-APR-1991; 91US-0681242.
 PR 22-NOV-1995; 95US-0562311.
 XX
 PA (KARM-) KARMANOS CANCER INST BARBARA ANN.
 XX
 PI Raz A;
 XX
 DR WPI: 1998-494766/42.
 DR N-PSDB; AAV54735.
 XX
 PT Test for metastatic potential of cell sample - by measuring binding
 of antibody to L-31-gal-lectin on cell surface
 XX
 PS Claim 1: Fig 6A-B; 24pp; English.
 XX
 CC The present sequence represents a beta-D-galactoside-binding protein
 designated L-31-gal-lectin. The sequence is derived from clone 1. The
 CC specification describes a method for testing a cell sample for
 CC metastatic potential. The method comprises contacting the sample with
 CC a labelled antibody that binds to endogenous cell-surface
 CC L-31-gal-lectin, removing unbound antibody, and determining the amount
 CC of bound antibody as a measure of L-31-gal-lectin expression, where the
 CC metastatic potential increases as the level of L-31-gal-lectin
 CC expression increases. The antibody is produced by immunisation with a
 CC L-31-gal-lectin protein.
 XX
 SQ Sequence 250 AA;
 Query Match 96.2%; Score 1305; DB 19; Length 250;
 Best Local Similarity 97.6%; Pred. No. 8e-96;
 Matches 244; Conservative 0; Mismatches 2; Indels 4; Gaps 4;
 Qy 1 MADNFSLDALSGSGNPNPQGWPGWAGNQAGAGYPGASYPG-YPGQAPPGAYPGQAPP 59
 Db 1 MADNFSLDALSGSGNPNPQGWPGWAGNQAGAGYPGASYPGAYPGQAPPGAYPGQAPP 60
 Qy 60 GAYHAGPAGYPCAPAGYVPGPPSPGAYPSSGQPSAPGAY-ATGPGYCAPAGPLIVPNL 118
 Db 61 GAYHAGPAGYPCAPAGYVPGPPSPGAYPSSGQPSAPGAYPATGPGYCAPAGPLIVPNL 120
 Qy 119 PLPGGVPRMLITILGTVKPNANRIALDFQGNDAVFHF-PFENNRRRVIVCNKLDNN 177
 Db 121 PLPGGVPRMLITILGTVKPNANRIALDFQGNDAVFHFENFRFENNRRRVIVCNKLDNN 180
 Qy 178 WGREERQSVFFPSGKPKFIQVLPEPDHFKVAVNDAH-LOYNHRVKKLNKLSIGSDI 236
 Db 181 WGREERQSVFFPSGKPKFIHVLPEPDHFKVAVNDAHLLQYNHRVKKLNKIRKLGISDI 240
 Qy 237 DLTSASYTMI 246
 Db 241 DLTSASYTMI 250
 RESULT 4
 AAU97818
 ID AAU97818 standard; Protein: 250 AA.

XX AAU97818;
 AC 27-AUG-2002 (first entry)
 DT
 DE Human cell membrane anchor protein galectin-3 #3.
 XX
 KW Galectin-3; cell membrane anchor protein; Ras; antisense technology;
 KW farnesylated isoform; H-Ras; K-Ras 4A; K-Ras 4B; N-Ras;
 KW mitosis disorder; cancer; non-malignancy; autoimmune disease;
 KW type 1 diabetes; lupus; multiple sclerosis; cirrhosis; graft rejection;
 KW atherosclerosis; polycystic kidney; post-angioplasty restenosis;
 KW cytostatic; immunosuppressive; antidiabetic; antiatherosclerotic;
 KW neuroprotective; vasotropic; hepatotropic; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200229031-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 01-OCT-2001; 2001WO-IL00918.
 XX
 PR 04-OCT-2000; 2000US-237858P.
 XX
 PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
 XX
 PI Klooq Y, Haklai R, Paz A, El Ad-Sfadia G, Ballan E;
 XX
 DR WPI: 2002-435333/46.
 XX
 PT Identifying anchor proteins that bind Ras protein, by producing
 complexes of Ras and cell membrane proteins in the presence and absence
 of a Ras antagonist and identifying a complex disrupted by the Ras
 antagonist
 XX
 PS Disclosure: Page 13; 62pp; English.
 XX
 CC The invention describes a method of identifying cell membrane anchor
 proteins that bind a Ras protein, involving preparing 2 reaction mixtures
 where one mixture has a Ras antagonist. A cross linking agent is added,
 and complexes between Ras protein and other proteins are produced. The
 complexes are then separated and the proteins binding to Ras are
 identified. The invention also describes a method useful for identifying
 drug candidates that inhibit aberrant Ras activity. An antisense compound
 comprising at least one phosphorothioate-modified nucleotide is useful
 for disrupting aberrant Ras activity in vivo, by infusing the antisense
 compound into a patient exhibiting this problem. The method is also
 useful for identifying anchor proteins for the farnesylated isoforms of
 H-Ras, K-Ras 4A, K-Ras 4B and N-Ras, whose mutated forms are known to be
 oncogenic. Reducing or inhibiting aberrant Ras activity in vivo is useful
 for treating diseases characterised by uncontrolled mitosis, including
 cancers and various non-malignancies such as autoimmune disease (e.g.
 type 1 diabetes, lupus and multiple sclerosis), cirrhosis, graft
 rejection, atherosclerosis, polycystic kidneys and post-angioplasty
 restenosis. This sequence encodes a galectin-3, a cell-membrane anchor
 protein that binds an isoform of Ras.
 XX
 SQ Sequence 250 AA;
 Query Match 96.2%; Score 1305; DB 23; Length 250;
 Best Local Similarity 98.0%; Pred. No. 8e-96;
 Matches 245; Conservative 0; Mismatches 1; Indels 4; Gaps 4;
 Qy 1 MADNFSLDALSGSGNPNPQGWPGWAGNQAGAGYPGASYPG-YPGQAPPGAYPGQAPP 59
 Db 1 MADNFSLDALSGSGNPNPQGWPGWAGNQAGAGYPGASYPGAYPGQAPPGAYPGQAPP 60
 Qy 60 GAYHAGPAGYPCAPAGYVPGPPSPGAYPSSGQPSAPGAY-ATGPGYCAPAGPLIVPNL 118
 Db 61 GAYHAGPAGYPCAPAGYVPGPPSPGAYPSSGQPSAPGAYPATGPGYCAPAGPLIVPNL 120
 Qy 119 PLPGGVPRMLITILGTVKPNANRIALDFQGNDAVFHF-PFENNRRRVIVCNKLDNN 177

Db	121	PLGCVVPRMLITILGTVPANRRALTDFQGNDAVFHFNFRNRRVIVCNKLDNN	180
Qy	178	WGREQSVFPFSGPKFKIQVLVPDHFVKVAVNDAH-LQYNHRVKKLNEISKLGISGDI	236
Db	181	WGREQSVFPFSGPKFKIQVLVPDHFVKVAVNDAHLLQYNHRVKKLNEISKLGISGDI	240
Qy	237	DLTSASVTMI	246
Db	241	DLTSASVTMI	250
Db	27-AUG-2002	(first entry)	
DE	Human cell membrane anchor protein galectin-3 #1.		
XX			
KW	Galectin-3; cell membrane anchor protein; Ras; antisense technology;		
KW	farnesylated isoform; H-Ras; K-Ras 4A; K-Ras 4B; N-Ras;		
KW	mitosis disorder; cancer; non-malignancy; autoimmune disease;		
KW	type 1 diabetes; lupus; multiple sclerosis; cirrhosis; graft rejection;		
KW	atherosclerosis; polycystic kidney; post-angioplasty restenosis;		
KW	cytostatic; immunosuppressive; anticatabolic; antiatherosclerotic;		
KW	neuroprotective; vasotropic; hepatotropic; human.		
XX			
XX	Homo sapiens.		
XX			
WO	20020229031-A2.		
PN			
XX			
PD	11-APR-2002.		
XX			
PF	01-OCT-2001; 2001WO-IL00918.		
XX			
PR	04-OCT-2000; 2000US-237858P.		
XX			
PA	(UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.		
PI	Kloog Y, Haklai R, Paz A, El Ad-Sfadia G, Ballan E;		
XX			
DR	WPI; 2002-435333/46.		
XX	N-PSDB; ABK52348.		
XX			
PT	Identifying anchor proteins that bind Ras protein, by producing		
PT	complexes of Ras and cell membrane proteins in the presence and absence		
PT	of a Ras antagonist and identifying a complex disrupted by the Ras		
PT	antagonist		
XX			
PS	Disclosure; Page 11-12; 62pp; English.		
XX			
CC	The invention describes a method of identifying cell membrane anchor		
CC	proteins that bind a Ras protein, involving preparing 2 reaction mixtures		
CC	where one mixture has a Ras antagonist. A cross linking agent is added,		
CC	and complexes between Ras protein and other proteins are produced. The		
CC	complexes are then separated and the proteins binding to Ras are		
CC	identified. The invention also describes a method useful for identifying		
CC	drug candidates that inhibit aberrant Ras activity. An antisense compound		
CC	comprising at least one phosphorothioate-modified nucleotide is useful		
CC	for disrupting aberrant Ras activity in vivo, by infusing the antisense		
CC	compound into a patient exhibiting this problem. The method is also		
CC	useful for identifying anchor proteins for the farnesylated isoforms of		
CC	H-Ras, K-Ras 4A, K-Ras 4B and N-Ras, whose mutated forms are known to be		
CC	oncogenic. Reducing or inhibiting aberrant Ras activity in vivo is useful		
CC	for treating diseases characterised by uncontrolled mitosis, including		
CC	cancers and various non-malignancies such as autoimmune disease (e.g.		
CC	type 1 diabetes, lupus and multiple sclerosis), cirrhosis, graft		
CC	rejection, atherosclerosis, polycystic kidneys and post-angioplasty		
CC	restenosis. This sequence encodes a galectin-3, a cell-membrane anchor		
CC	protein that binds an isoform of Ras.		

Db	117	AAGPYGVPAAGLAVPYDPLPGGVMPRLITMGTVKPNANRVLVDFRGRNDVAFHFNPR	178			
QY	160	FNENRRVIVCNTKLDNNWGREERQSFPPESGPKFKIQVLVPDHFVKVAVNDAH-LOYN	218			
Db	177	FNENRRVIVCNTKQDNNWCKEERQSAFPESGPKFKIQVLVEADHFVKVAVNDAHLLQYN	236			
QY	219	HRVKKLNEISKLGISGDIDLTLSASYTM	246			
Db	237	HRMKNLREISQLGISGDITLTSANHAMI	264			
RESULT 11						
AAR13338						
ID	AAR13338 standard; Protein; 278 AA.					
XX	AAR13338;					
XX	XX					
DT	12-SEP-1991 (first entry)					
XX	Mac-2 protein including putative signal sequence.					
DE	HMEBP; leishmaniasis; Mouse Mac-2; laminin.					
XX	Mus musculus.					
OS	XX					
XX	XX					
FH	Key Location/Qualifiers					
FT	Peptide 1..14					
FT	/label= putative signal peptide					
FT	/note= "Met(1) is encoded by CTC"					
FT	Protein 15..278					
FT	/label= Mac-2					
XX	XX					
PN	W09108290-A.					
XX	XX					
PD	13-JUN-1991.					
XX	XX					
PF	29-NOV-1990; 90WO-US06948.					
XX	XX					
PK	14-SEP-1990; 90US-0582628.					
PR	30-NOV-1989; 89US-0444195.					
XX	XX					
PA	(GEHO-) GEN HOSPITAL CORP.					
XX	XX					
PI	Pillai S, Cherayil BJ;					
XX	XX					
DR	WPI; 1991-193196/26.					
DR	N-PSDB; AAO12210.					
XX	XX					
PT	Recombinant gene encoding human macrophage carbohydrate -					
PT	Ige-binding protein and antibody used to treat, diagnose and					
PT	prevent e.g. inflammatory bowel disorder, leishmaniasis, hayfever					
PT	and bronchial					
XX	XX					
PS	Disclosure; Fig 2D; 36pp; English.					
XX	XX					
CC	This sequence is identical to that deduced from clone Mac 2.16 (see					
CC	AAR1531, except for the putative signal peptide. Mac 2.16 itself					
CC	does not encode a signal peptide, but Mac-2 protein newly synthesised					
CC	by mouse inflammatory peritoneal macrophages was detected in the					
CC	extracellular medium. Clone Mac 2.9 (from which this sequence was					
CC	deduced) was thus analysed for presence of a signal sequence.					
CC	See also AAO12207 (for Mac 2.16), AAO12209, AAO12211.					
XX	XX					
SQ	Sequence 278 AA;					
Query Match 79.7%; Score 1082; DB 12; Length 278;						
Best Local Similarity 78.0%; Pred. No. 4.3e-78;						
Matches 209; Conservative 16; Mismatches 17; Indels 26; Gaps						
QY	1 MADNFSLDALSGCNPNPGCWPGWGNQAGAGTGGASYPG-YFCQAPPAYPGQAPP					
Db	15 MADSFSLDALSGNPNPGYFGWGNQ-P-GAGGYPGAYPGAYPGQAPPAYPGQAPP					

QY 60 GAYHG-----APGAYGPAPGVYPPSGPGAYSSGQSPAPGAY----- 100
 DB 74 GATPGQAPPAYPGTAPGAYPGTAPGAYPGQA-PGAPP--GQPCAPGAYPQCSGGYP 130
 QY 101 ATGPGAPAGPLIVPNLPLPGGVVPRMLITILGTVPKPNANRIALDFQGNDAVAFHF-PR 159
 DB 131 AAGPGYGPAGPLVYDPLPLPGGVVPRMLITILGTVPKPNANRIALDFQGNDAVAFHF-PR 190
 QY 160 FNNRRVIVCNTKLDNNWGREERQSPFPESGKPKIOVLVEADHFKVAVNDAAH-LQYN 218
 DB 191 FNNRRVIVCNTKLDNNWGREERQSPFPESGKPKIOVLVEADHFKVAVNDAAHLLQYN 250
 QY 219 HRVKKLNEISKLISGIDILTSASYMI 246
 DB 251 HRMKNLREISQLISGIDILTSANHAMI 278
 RESULT 12
 AAU97821
 ID AAU97821 standard; Protein; 262 AA.
 XX
 AC AAU97821;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Rat cell membrane anchor protein galectin-3.
 XX
 KW Galectin-3; cell membrane anchor protein; Ras; antisense technology;
 KW farnesylated isoform; H-Ras; K-Ras 4A; K-Ras 4B; N-Ras;
 KW mitosis disorder; cancer; non-malignancy; autoimmune disease;
 KW type 1 diabetes; lupus; multiple sclerosis; cirrhosis; graft rejection;
 KW atherosclerosis; polycystic kidney; post-angioplasty restenosis;
 KW cytostatic; immunosuppressive; antidiabetic; antiatherosclerotic;
 KW neuroprotective; vasotropic; hepatotropic; rat.
 XX
 OS Rattus sp.
 XX
 PN WO200229031-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 01-OCT-2001; 2001WO-IL00918.
 XX
 PR 04-OCT-2000; 2000US-237858P.
 XX
 PA (UVRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
 XX
 PI Klooog Y, Haklai R, Paz A, El Ad-Sfadia G, Ballan E;
 XX
 DR WPI; 2002-435333/46.
 XX
 XX Identifying anchor proteins that bind Ras protein, by producing
 PT complexes of Ras and cell membrane proteins in the presence and absence
 PT of a Ras antagonist and identifying a complex disrupted by the Ras
 PT antagonist
 XX
 PS Disclosure; Page 14; 62pp; English.
 XX
 CC The invention describes a method of identifying cell membrane anchor
 CC proteins that bind a Ras protein, involving preparing 2 reaction mixtures
 CC where one mixture has a Ras antagonist. A cross linking agent is added,
 CC and complexes between Ras protein and other proteins are produced. The
 CC complexes are then separated and the proteins binding to Ras are
 CC identified. The invention also describes a method useful for identifying
 CC drug candidates that inhibit aberrant Ras activity. An antisense compound
 CC comprising at least one phosphorothioate-modified nucleotide is useful
 CC for disrupting aberrant Ras activity in vivo, by infusing the antisense
 CC compound into a patient exhibiting this problem. The method is also
 CC useful for identifying anchor proteins for the farnesylated isoforms of
 CC H-Ras, K-Ras 4A, K-Ras 4B and N-Ras, whose mutated forms are known to be
 CC oncogenic. Reducing or inhibiting aberrant Ras activity in vivo is useful
 CC for treating diseases characterised by uncontrolled mitosis, including
 CC cancers and various non-malignancies such as autoimmune disease (e.g.

CC type 1 diabetes, lupus and multiple sclerosis), cirrhosis, graft
 CC rejection, atherosclerosis, polycystic kidneys and post-angioplasty
 CC restenosis. This sequence encodes a galectin-3, a cell-membrane anchor
 CC protein that binds an isoform of Ras.
 XX
 SQ Sequence 262 AA;
 Query Match 79.5%; Score 1079; DB 23; Length 262;
 Best Local Similarity 77.9%; Pred. No. 7e-78;
 Matches 205; Conservative 16; Mismatches 24; Indels 18; Gaps 7;
 QY 1 MADNLSLHDLSSGNPNQGWPGWAGNPGAGAGGYPGASYPG-YPGQAPPAGYPGQAPP 59
 DB 1 MADGFSLDALAGSGNPNQGWPGWAGNQP-GAGGYPGASYPGAGYPGQAPP 59
 QY 60 GAYHG-----APGAYGPAPGVYPPSGPGAYPSS--GQSPAPGAY-ATGYPY 105
 DB 60 SAYPGTGPSAYPGTAPGAYPGTAPGAYPGQPGGPGAYPSAPGAYPATGPF 119
 QY 106 GAPAGPLIVPNLPLPGGVVPRMLITILGTVPKPNANRIALDFQGNDAVAFHF-PRFENN 164
 DB 120 GAPTGPLTVYDPLPLPGGVVPRMLITILGTVPKPNANSITLNFKKGNDIAFHFNPRFENN 179
 QY 165 RRIVVNTKLDNNWGREERQSPFPESGKPKIOVLVEADHFKVAVNDAAH-LQYNHRVK 223
 DB 180 RRIVVNTKLDNNWGREERQSPFPESGKPKIOVLVEADHFKVAVNDVHLLQYNHRMKN 239
 QY 224 LNEISKLISGIDILTSASYMI 246
 DB 240 LREISQLISGIDILTSASHAMI 262
 RESULT 13
 AAU71219
 ID AAU71219 standard; Protein; 264 AA.
 XX
 AC AAU71219;
 XX
 DT 30-OCT-1998 (first entry)
 XX
 DE Beta-D-galactoside-binding protein designated L-31-gal-lectin.
 XX
 KW Beta-D-galactoside-binding protein; L-31-gal-lectin;
 KW metastatic potential; antibody.
 XX
 OS Homo sapiens.
 XX
 PN US5801002-A.
 XX
 PD 01-SEP-1998.
 XX
 PF 22-NOV-1995; 95US-0562311.
 XX
 PR 26-JAN-1994; 94US-0188225.
 PR 06-JAN-1989; 89US-0294249.
 PR 05-APR-1991; 91US-0681242.
 PR 22-NOV-1995; 95US-0562311.
 XX
 PA (KARM-) KARMANOS CANCER INST BARBARA ANN.
 XX
 PI Raz A;
 XX
 DR WPI; 1998-494766/42.
 DR N-PSDB; AAV34736.
 XX
 XX Test for metastatic potential of cell sample - by measuring binding
 PT of antibody to L-31-gal-lectin on cell surface
 XX
 PS Disclosure; Fig 3A-B; 24pp; English.
 XX
 CC The present sequence represents a beta-D-galactoside-binding protein
 CC designated L-31-gal-lectin. The sequence is derived from clone 2. The
 CC specification describes a method for testing a cell sample for

CC where one mixture has a Ras antagonist. A cross linking agent is added,
CC and complexes between Ras protein and other proteins are produced. The
CC complexes are then separated and the proteins binding to Ras are
CC identified. The invention also describes a method useful for identifying
CC drug candidates that inhibit aberrant Ras activity. An antisense compound
CC comprising at least one phosphorothioate-modified nucleotide is useful
CC for disrupting aberrant Ras activity in vivo, by infusing the antisense
CC compound into a patient exhibiting this problem. The method is also
CC useful for identifying anchor proteins for the farnesylated isoforms of
CC H-Ras, K-Ras 4A, K-Ras 4B and N-Ras, whose mutated forms are known to be
CC oncogenic. Reducing or inhibiting aberrant Ras activity in vivo is useful
CC for treating diseases characterised by uncontrolled mitosis, including
CC cancers and various non-malignancies such as autoimmune disease (e.g.
CC type 1 diabetes, lupus and multiple sclerosis), cirrhosis, graft
CC rejection, atherosclerosis, polycystic kidneys and post-angioplasty
CC restenosis. This sequence encodes a galectin-3, a cell-membrane anchor
CC protein that binds an isoform of Ras.

xx
SQ Sequence 263 AA;

Query Match 78.4%; Score 1064.5; DB 23; Length 263;
Best Local Similarity 77.6%; Pred. No. 9.9e-77;
Matches 208; Conservative 16; Mismatches 17; Indels 27; Gaps 9;

QY 1 MADNFSLDALSGSGNPNQGWPGWAGNQAGAGYPCASYPG-YPCQAPPGAYPGQAPP 59
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 MADSFLNDALAGSGNPNQGYPGWGNQ-P-GAGGYPGAAYPGAYPGQAPP 59
QY 60 GAYHG-----APGAYPGAPAGVYPPGPGPGAYPSSGQPSAPGAY----- 100
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
60 GAYPGQAPPAYPGCTAPGAYPGTAPGAYPGQPA-PGAPP--GQPGAPGAYPCSCGGYP 116
QY 101 ATGPGYAPAGPLIYVYNLPLPGGVYPRMLITILGTVPNANRIALDFQGNDAFHF-PR 159
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
117 AAGP-GVPAGPLTPYDPLPLPGGVMPRLITINGTVKPNANRIVLDFRGNDAFHNPR 175
QY 160 FNNNRRVIVCNTKLDNNWGREERQSVFPESGKPFKIQVLVEPDHFKVAVNDAH-LOYN 218
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
176 FNNNRRVIVCNTKQDNNWGREERQSAFPESGKPFKIQVLVEADHFKVAVNDAHLQYN 235
QY 219 HRVKKLNEISKIGISGDILTSASYMI 246
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
236 HRMKNLREISQLISGDITLTSANHAMI 263

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 Quantitative thresholds of MHC class II I-E expressed on hemopoietically derived antigen-presenting cells in transgenic NOD/Lt mice determine level of diabetes resistance and indicate mechanism of protection.
 J Immunol. 1996 Aug 1;157(3):1279-87.
 PMID: 8757636 [PubMed - indexed for MEDLINE]
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 Altered ovarian sterol carrier protein expression in the pregnant streptozotocin-treated diabetic rat.
 Biol Reprod. 1996 Jul;55(1):38-46.
 PMID: 8793056 [PubMed - indexed for MEDLINE]
- ☐ 3: [Laville M, Auboeuf D, Khalfallah Y, Vega N, Riou JP, Vidal H.](#) [Related Articles](#), [Links](#)
 Acute regulation by insulin of phosphatidylinositol-3-kinase, Rad, Glut 4, and lipoprotein lipase mRNA levels in human muscle.
 J Clin Invest. 1996 Jul 1;98(1):43-9.
 PMID: 8690802 [PubMed - indexed for MEDLINE]
- ☐ 4: [Taniguchi N, Kaneto H, Asahi M, Takahashi M, Wenyi C, Higashiyama S, Fujii J, Suzuki K, Kayanoki Y.](#) [Related Articles](#), [Links](#)
 Involvement of glycation and oxidative stress in diabetic macroangiopathy.
 Diabetes. 1996 Jul;45 Suppl 3:S81-3.
 PMID: 8674900 [PubMed - indexed for MEDLINE]
- ☐ 5: [Tsao TS, Burcelin R, Charron MJ.](#) [Related Articles](#), [Links](#)
 Regulation of hexokinase II gene expression by glucose flux in skeletal muscle.
 J Biol Chem. 1996 Jun 21;271(25):14959-63.
 PMID: 8663067 [PubMed - indexed for MEDLINE]
- ☐ 6: [Vafiadis P, Bennett ST, Colle E, Grabs R, Goodyer CG, Polychronakos C.](#) [Related Articles](#), [Links](#)
 Imprinted and genotype-specific expression of genes at the IDDM2 locus in pancreas and leucocytes.
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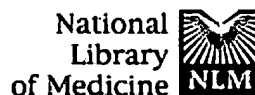
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